GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 00:31:12 ; Search time 119.491 Seconds
(without alignments)
96.991 Million cell updates/sec

Title: US-10-688-489-59
Perfect score: 31
Sequence: 1 tccgccaccggaagttgagtagacggtgctg 31

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	30	96.8	11029	6	US-10-714-781A-66	Sequence 66, Appl
	2	20.4	65.8	164527	7	US-11-121-086-71	Sequence 71, Appl
c	3	18.4	59.4	750	7	US-11-056-825-3	Sequence 3, Appli
c	4	18.4	59.4	750	7	US-11-056-825-6	Sequence 6, Appli
	5	17.4	56.1	1130	7	US-11-000-463-488	Sequence 488, App
	6	17.4	56.1	1557	6	US-10-750-185-33268	Sequence 33268, A
	7	17.4	56.1	1600	7	US-11-000-463-16	Sequence 16, Appl
	8	17.4	56.1	2891	6	US-10-821-234-84	Sequence 84, Appl
c	9	17.2	55.5	1395	7	US-11-055-822-1035	Sequence 1035, Ap
c	10	17.2	55.5	1082144	7	US-11-117-187-211	Sequence 211, App
c	11	17	54.8	777	6	US-10-512-184-9	Sequence 9, Appli
c	12	17	54.8	1113	6	US-10-512-184-60	Sequence 60, Appl
c	13	17	54.8	1881	6	US-10-512-184-24	Sequence 24, Appl
c	14	16.8	54.2	2313	7	US-11-000-365-51	Sequence 51, Appl
c	15	16.8	54.2	2313	7	US-11-032-794-51	Sequence 51, Appl
	16	16.8	54.2	175673	7	US-11-121-086-55	Sequence 55, Appl
	17	16.6	53.5	862	6	US-10-750-185-37736	Sequence 37736, A
c	18	16.6	53.5	1413	7	US-11-055-822-959	Sequence 959, App
	19	16.6	53.5	1571	6	US-10-750-185-34369	Sequence 34369, A
c	20	16.6	53.5	1726	6	US-10-750-185-35332	Sequence 35332, A
c	21	16.6	53.5	1804	6	US-10-750-185-31994	Sequence 31994, A
	22	16.6	53.5	149419	7	US-11-112-908-49	Sequence 49, Appl
	23	16.6	53.5	157224	7	US-11-112-908-51	Sequence 51, Appl
	24	16.6	53.5	161726	7	US-11-112-908-48	Sequence 48, Appl
	25	16.6	53.5	161726	7	US-11-112-908-52	Sequence 52, Appl
c	26	16.6	53.5	178877	7	US-11-121-086-17	Sequence 17, Appl
	27	16.4	52.9	156297	7	US-11-121-086-65	Sequence 65, Appl
c	28	16.4	52.9	171423	7	US-11-121-086-85	Sequence 85, Appl
c	29	16.4	52.9	175416	7	US-11-121-086-43	Sequence 43, Appl
c	30	16.2	52.3	600	6	US-10-750-185-507	Sequence 507, App
	31	16.2	52.3	600	6	US-10-750-185-1980	Sequence 1980, Ap
	32	16.2	52.3	699	6	US-10-750-185-47086	Sequence 47086, A
	33	16.2	52.3	981	6	US-10-858-730-136	Sequence 136, App
	34	16.2	52.3	2356	6	US-10-750-185-46730	Sequence 46730, A
	35	16.2	52.3	3138	6	US-10-392-234A-15	Sequence 15, Appl
c	36	16.2	52.3	3187	6	US-10-821-234-69	Sequence 69, Appl
	37	16.2	52.3	3336	6	US-10-750-185-45825	Sequence 45825, A
	38	16.2	52.3	162289	7	US-11-121-086-20	Sequence 20, Appl
c	39	16	51.6	438	7	US-11-012-353-51	Sequence 51, Appl
c	40	16	51.6	3754	6	US-10-750-185-48934	Sequence 48934, A
	41	16	51.6	184000	7	US-11-121-086-37	Sequence 37, Appl
c	42	15.8	51.0	855	6	US-10-750-185-56888	Sequence 56888, A
c	43	15.8	51.0	1632	6	US-10-750-185-38126	Sequence 38126, A
c	44	15.8	51.0	1741	7	US-11-000-463-97	Sequence 97, Appl
	45	15.8	51.0	2134	6	US-10-750-185-57401	Sequence 57401, A

ALIGNMENTS

RESULT 1
US-10-714-781A-66
; Sequence 66, Application US/10714781A
; Publication No. US20050255127Ai
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: MINKE, JULES MAARTEN
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
; FILE REFERENCE: 574313-3161.5
; CURRENT APPLICATION NUMBER: US/10/714,781A
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 10/679,520
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: 10/374,953
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 10/116,298
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,923
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 10/676,502
; PRIOR FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: PCT/FR02/01200
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(10395)
US-10-714-781A-66

Query Match 96.8%; Score 30; DB 6; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.00019;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              ||||||||||||||||||||||||||||||
Db      10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552
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RESULT 2
US-11-121-086-71
; Sequence 71, Application US/11121086

; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 71
; LENGTH: 164527
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-71

Query Match 65.8%; Score 20.4; DB 7; Length 164527;
Best Local Similarity 80.0%; Pred. No. 5.2;
Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
|| |||||||||||||| ||| | || ||
Db 66059 CCCTCACCGGAAGTTGAGGAGATGCTGGTG 66088

RESULT 3
US-11-056-825-3/c
; Sequence 3, Application US/11056825
; Publication No. US20050255109A1
; GENERAL INFORMATION:
; APPLICANT: Felding-Habermann, Brunhilde
; APPLICANT: Janda, Kim D.
; APPLICANT: Saven, Alan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
; FILE REFERENCE: SCRP-0042
; CURRENT APPLICATION NUMBER: US/11/056,825
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/626,726
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/544,807
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(750)
US-11-056-825-3

Query Match 59.4%; Score 18.4; DB 7; Length 750;
Best Local Similarity 78.6%; Pred. No. 21;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAGTTGAGTAGACGGTG 28
|||||||||| |||| ||||||||
Db 375 TCCGCCACCGCCGCCTGAGGAGACGGTG 348

RESULT 4
US-11-056-825-6/c
; Sequence 6, Application US/11056825
; Publication No. US20050255109A1
; GENERAL INFORMATION:
; APPLICANT: Felding-Habermann, Brunhilde
; APPLICANT: Janda, Kim D.
; APPLICANT: Saven, Alan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF METASTASIS
; FILE REFERENCE: SCRP-0042
; CURRENT APPLICATION NUMBER: US/11/056,825
; CURRENT FILING DATE: 2005-02-11
; PRIOR APPLICATION NUMBER: US 60/626,726
; PRIOR FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/544,807
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 750
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-11-056-825-6

Query Match 59.4%; Score 18.4; DB 7; Length 750;
Best Local Similarity 78.6%; Pred. No. 21;
Matches 22; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAGTTGAGTAGACGGTG 28
|||||||||| |||| ||||||||
Db 375 TCCGCCACCGCCGCCTGAGGAGACGGTG 348

RESULT 5
US-11-000-463-488
; Sequence 488, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 488
; LENGTH: 1130
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-000-463-488

Query Match 56.1%; Score 17.4; DB 7; Length 1130;
Best Local Similarity 77.8%; Pred. No. 63;
Matches 21; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          5 CCACCGGAAGTTGAGTAGACGGTGCTG 31
              |||| |||||   || ||| |||||||
Db        387 CCACGGGAAGGACAGGAGAAGGTGCTG 413


RESULT 6
US-10-750-185-33268
; Sequence 33268, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 33268
;   LENGTH: 1557
;   TYPE: DNA
;   ORGANISM: Bovine  19866880342191
US-10-750-185-33268

  Query Match             56.1%;  Score 17.4;  DB 6;  Length 1557;
  Best Local Similarity   77.8%;  Pred. No. 66;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 CGCCACCGGAAGTTGAGTAGACGGTGC 29
              | ||| ||||| |  ||||||| ||||
Db       1357 CTCCAGCGGAATTGAAGTAGACAGTGC 1383


RESULT 7
US-11-000-463-16
; Sequence 16, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Chen, Rui-hong
;  APPLICANT:  Qian, Xiaohong B.
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Cao, Yi-Cheng
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
;  FILE REFERENCE: 785CIP4CN
;  CURRENT APPLICATION NUMBER: US/11/000,463
;  CURRENT FILING DATE:  2004-11-29
;  PRIOR APPLICATION NUMBER: 10/291,265
;  PRIOR FILING DATE: 2002-11-08
;  PRIOR APPLICATION NUMBER: PCT/US01/02623
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 09/922,279
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 09/617,746
;  PRIOR FILING DATE: 2000-07-17
;  PRIOR APPLICATION NUMBER: 09/631,451
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: 09/633,870
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 944
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 1600
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (242)..(589)
US-11-000-463-16

  Query Match             56.1%;  Score 17.4;  DB 7;  Length 1600;
  Best Local Similarity   77.8%;  Pred. No. 66;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          5 CCACCGGAAGTTGAGTAGACGGTGCTG 31
              |||| |||||   || ||| |||||||
Db        387 CCACGGGAAGGACAGGAGAAGGTGCTG 413


RESULT 8
US-10-821-234-84
; Sequence 84, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 84
;   LENGTH: 2891
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-821-234-84

  Query Match             56.1%;  Score 17.4;  DB 6;  Length 2891;
  Best Local Similarity   77.8%;  Pred. No. 71;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          5 CCACCGGAAGTTGAGTAGACGGTGCTG 31
              ||| ||||||  ||   ||||||||||
Db        189 CCATCGGAAGACGATGGGACGGTGCTG 215


RESULT 9
US-11-055-822-1035/c
; Sequence 1035, Application US/11055822
; Publication No. US20050260707A1
; GENERAL INFORMATION:
;  APPLICANT: Pompejus, Markus
;  APPLICANT:  Kroger, Burkhard
;  APPLICANT:  Schroder, Hartwig
;  APPLICANT:  Zelder, Oskar
;  APPLICANT:  Haberhauer, Gregor
;  TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
;  TITLE OF INVENTION:  METABOLIC PATHWAY PROTEINS
;  FILE REFERENCE: BGI-121CPCN
;  CURRENT APPLICATION NUMBER: US/11/055,822
;  CURRENT FILING DATE:  2005-02-11
;  PRIOR APPLICATION NUMBER: 09/606,740
;  PRIOR FILING DATE: 2000-06-23
;  PRIOR APPLICATION NUMBER: 60/141,031
;  PRIOR FILING DATE: 1999-06-25
;  PRIOR APPLICATION NUMBER: 60/142,101
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;  PRIOR FILING DATE: 1999-07-02
;  PRIOR APPLICATION NUMBER: 60/148,613
;  PRIOR FILING DATE: 1999-08-12
;  PRIOR APPLICATION NUMBER: 60/187,970
;  PRIOR FILING DATE: 2000-03-09
;  PRIOR APPLICATION NUMBER: DE 19930476.9
;  PRIOR FILING DATE: 1999-07-01
;  PRIOR APPLICATION NUMBER: DE 19931415.2
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931418.7
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931419.5
;  PRIOR FILING DATE: 1999-07-08
;  PRIOR APPLICATION NUMBER: DE 19931420.9
;  PRIOR FILING DATE: 1999-07-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1158
; SEQ ID NO 1035
;   LENGTH: 1395
;   TYPE: DNA
;   ORGANISM: Corynebacterium glutamicum
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (101)..(1372)
;   OTHER INFORMATION: RXA01483
US-11-055-822-1035

  Query Match            55.5%;  Score 17.2;  DB 7;  Length 1395;
  Best Local Similarity   73.3%;  Pred. No. 80;
  Matches   22;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              || ||||||||||||      ||| |||||
Db        917 CCACCACCGGAAGTTCCCGCAACGATGCTG 888


RESULT 10
US-11-117-187-211/c
; Sequence 211, Application US/11117187
; Publication No. US20050266560A1
; GENERAL INFORMATION:
;  APPLICANT: PREUSS, DAPHNE
;  APPLICANT:  COPENHAVER, GREGORY
;  TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
;  FILE REFERENCE: ARCD:309US
;  CURRENT APPLICATION NUMBER: US/11/117,187
;  CURRENT FILING DATE:  2005-04-28
;  PRIOR APPLICATION NUMBER: US/09/531,120
;  PRIOR FILING DATE: 2000-03-17
;  PRIOR APPLICATION NUMBER: 60/125,219
;  PRIOR FILING DATE: 1999-03-18
;  NUMBER OF SEQ ID NOS: 212
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 211
;   LENGTH: 1082144
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-11-117-187-211

  Query Match            55.5%;  Score 17.2;  DB 7;  Length 1082144;
  Best Local Similarity   86.4%;  Pred. No. 1.4e+02;
  Matches   19;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 TCCGCCACCGGAAGTTGAGTAG 22
              |||  || ||||||||||||||
Db     364367 TCCCACATCGGAAGTTGAGTAG 364346


RESULT 11
US-10-512-184-9/c
; Sequence 9, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
;  APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
;  TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
;  TITLE OF INVENTION:  antibody fragments and fusions mediated plant disease
;  TITLE OF INVENTION:  resistance against fungi
;  FILE REFERENCE: 3581.01US01
;  CURRENT APPLICATION NUMBER: US/10/512,184
;  CURRENT FILING DATE:  2004-10-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 777
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
;   OTHER INFORMATION: specificity against Phoma lingam; originates from
;   OTHER INFORMATION: Mus musculus.
US-10-512-184-9

  Query Match            54.8%;  Score 17;  DB 6;  Length 777;
  Best Local Similarity   80.0%;  Pred. No. 91;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          7 ACCGGAAGTTGAGTAGACGGTGCTG 31
              ||| |||||| || |||| || |||
Db        593 ACCAGAAGTTTAGGAGACTGTCCTG 569


RESULT 12
US-10-512-184-60/c
; Sequence 60, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
;  APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
;  TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
;  TITLE OF INVENTION:  antibody fragments and fusions mediated plant disease
;  TITLE OF INVENTION:  resistance against fungi
;  FILE REFERENCE: 3581.01US01
;  CURRENT APPLICATION NUMBER: US/10/512,184
;  CURRENT FILING DATE:  2004-10-22
;  NUMBER OF SEQ ID NOS: 72
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
;   LENGTH: 1113
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: precursor
;   OTHER INFORMATION: fusion protein comprising ACE - linker - scFv PL2.
US-10-512-184-60

  Query Match            54.8%;  Score 17;  DB 6;  Length 1113;
  Best Local Similarity   80.0%;  Pred. No. 95;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          7 ACCGGAAGTTGAGTAGACGGTGCTG 31
              ||| |||||| || |||| || |||
Db        929 ACCAGAAGTTTAGGAGACTGTCCTG 905


RESULT 13
US-10-512-184-24/c
; Sequence 24, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
;  APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
;  TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
;  TITLE OF INVENTION:  antibody fragments and fusions mediated plant disease
;  TITLE OF INVENTION:  resistance against fungi
;  FILE REFERENCE: 3581.01US01
;  CURRENT APPLICATION NUMBER: US/10/512,184
;  CURRENT FILING DATE:  2004-10-22
;  NUMBER OF SEQ ID NOS: 72
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```
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 1881
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: fusion protein
;   OTHER INFORMATION: comprising leader peptide - chitinase - linker -
;   OTHER INFORMATION: scFv PL2 - cmyc/His6.
US-10-512-184-24

  Query Match             54.8%;  Score 17;  DB 6;  Length 1881;
  Best Local Similarity   80.0%;  Pred. No. 1e+02;
  Matches   20;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          7 ACCGGAAGTTGAGTAGACGGTGCTG 31
              ||| |||||| || |||| || |||
Db       1616 ACCAGAAGTTTAGGAGACTGTCCTG 1592


RESULT 14
US-11-000-365-51/c
; Sequence 51, Application US/11000365
; Publication No. US20050267022A1
; GENERAL INFORMATION:
;  APPLICANT: FRANZOSO, GUIDO
;  APPLICANT:  PAPA, SALVATORE
;  APPLICANT:  BUBICI, CONCETTA
;  APPLICANT:  DESMAELE, ENRICO
;  APPLICANT:  ZAZZERONI, FRANCESCA
;  TITLE OF INVENTION: IDENTIFICATION OF NOVEL FACTORS THAT BLOCK PROGRAMMED
;  TITLE OF INVENTION:  CELL DEATH OR APOPTOSIS BY TARGETING JNK
;  FILE REFERENCE: 21459-97705
;  CURRENT APPLICATION NUMBER: US/11/000,365
;  CURRENT FILING DATE:  2004-11-29
;  PRIOR APPLICATION NUMBER: 60/526,231
;  PRIOR FILING DATE: 2003-12-02
;  PRIOR APPLICATION NUMBER: 10/626,905
;  PRIOR FILING DATE: 2003-07-25
;  PRIOR APPLICATION NUMBER: 10/263,330
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/328,811
;  PRIOR FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: 60/326,492
;  PRIOR FILING DATE: 2001-10-02
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 51
;   LENGTH: 2313
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-000-365-51

  Query Match             54.2%;  Score 16.8;  DB 7;  Length 2313;
  Best Local Similarity   75.0%;  Pred. No. 1.3e+02;
  Matches   21;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 GCCACCGGAAGTTGAGTAGACGGTGCTG 31
              || ||| ||||  | | ||| |||||||
Db       1266 GCTACCTGAAGAAGGGCAGATGGTGCTG 1239


RESULT 15
US-11-032-794-51/c
; Sequence 51, Application US/11032794
; Publication No. US20050265970A1
; GENERAL INFORMATION:
;  APPLICANT: FRANZOSO, GUIDO
;  APPLICANT:  PAPA, SALVATORE
;  APPLICANT:  BUBICI, CONCETTA
;  APPLICANT:  DESMAELE, ENRICO
;  APPLICANT:  ZAZZERONI, FRANCESCA
;  TITLE OF INVENTION: IDENTIFICATION OF NOVEL FACTORS THAT BLOCK PROGRAMMED
;  TITLE OF INVENTION:  CELL DEATH OR APOPTOSIS BY TARGETING JNK
;  FILE REFERENCE: 21459-97816
;  CURRENT APPLICATION NUMBER: US/11/032,794
;  CURRENT FILING DATE:  2005-01-10
;  PRIOR APPLICATION NUMBER: 11/000,365
;  PRIOR FILING DATE: 2004-11-29
;  PRIOR APPLICATION NUMBER: 60/526,231
;  PRIOR FILING DATE: 2003-12-02
;  PRIOR APPLICATION NUMBER: 10/626,905
;  PRIOR FILING DATE: 2003-07-25
;  PRIOR APPLICATION NUMBER: 10/263,330
;  PRIOR FILING DATE: 2002-10-02
;  PRIOR APPLICATION NUMBER: 60/328,811
;  PRIOR FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: 60/326,492
;  PRIOR FILING DATE: 2001-10-02
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 51
;   LENGTH: 2313
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-11-032-794-51

  Query Match             54.2%;  Score 16.8;  DB 7;  Length 2313;
  Best Local Similarity   75.0%;  Pred. No. 1.3e+02;
  Matches   21;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          4 GCCACCGGAAGTTGAGTAGACGGTGCTG 31
              || ||| ||||  | | ||| |||||||
Db       1266 GCTACCTGAAGAAGGGCAGATGGTGCTG 1239


Search completed: December 12, 2005, 02:23:15
Job time : 120.491 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 11, 2005, 21:35:42 ; Search time 81.1636 Seconds
(without alignments)
678.930 Million cell updates/sec

Title: US-10-688-489-59
Perfect score: 31
Sequence: 1 tccgccaccggaagttgagtagacggtgctg 31

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	19.8	63.9	1806	3	US-09-252-991A-15978	Sequence 15978, A
	2	19.8	63.9	2289	3	US-09-252-991A-16301	Sequence 16301, A
	3	19.6	63.2	111	3	US-08-454-098-5	Sequence 5, Appli
	4	19.6	63.2	111	6	PCT-US96-01600-5	Sequence 5, Appli
c	5	19	61.3	436	3	US-09-464-535-13	Sequence 13, Appl
c	6	19	61.3	490	3	US-09-318-786-36	Sequence 36, Appl
c	7	19	61.3	600	3	US-09-464-535-39	Sequence 39, Appl
c	8	19	61.3	673	3	US-09-464-535-31	Sequence 31, Appl
c	9	19	61.3	1578	3	US-09-351-224E-7	Sequence 7, Appli
c	10	19	61.3	1578	3	US-09-677-488A-7	Sequence 7, Appli
c	11	19	61.3	1578	3	US-09-677-682B-7	Sequence 7, Appli
c	12	19	61.3	1578	3	US-09-882-694B-7	Sequence 7, Appli
c	13	19	61.3	1764	3	US-09-351-224E-6	Sequence 6, Appli
c	14	19	61.3	1764	3	US-09-677-488A-6	Sequence 6, Appli
c	15	19	61.3	1764	3	US-09-677-682B-6	Sequence 6, Appli
c	16	19	61.3	1764	3	US-09-882-694B-6	Sequence 6, Appli
c	17	18.8	60.6	1309	3	US-09-270-767-11451	Sequence 11451, A
c	18	18.8	60.6	1846	3	US-09-270-767-14186	Sequence 14186, A
	19	18.8	60.6	22761	3	US-09-902-540-1219	Sequence 1219, Ap
c	20	18.6	60.0	601	3	US-09-949-016-23874	Sequence 23874, A
c	21	18.6	60.0	601	3	US-09-949-016-197817	Sequence 197817,
c	22	18.6	60.0	601	3	US-09-949-016-197864	Sequence 197864,
	23	18.6	60.0	51927	3	US-09-949-016-17347	Sequence 17347, A
	24	18.6	60.0	51927	3	US-09-949-016-17348	Sequence 17348, A
	25	18.6	60.0	73853	3	US-09-949-016-12029	Sequence 12029, A
	26	18.4	59.4	49	2	US-08-726-528A-7	Sequence 7, Appli
c	27	18.4	59.4	601	3	US-09-949-016-52563	Sequence 52563, A
c	28	18.4	59.4	660	3	US-09-533-559-7236	Sequence 7236, Ap
c	29	18.4	59.4	668	3	US-09-533-559-6969	Sequence 6969, Ap
c	30	18.4	59.4	875	3	US-09-533-559-7730	Sequence 7730, Ap
c	31	18.2	58.7	720	2	US-08-459-354-3	Sequence 3, Appli
c	32	18.2	58.7	720	2	US-08-077-253-3	Sequence 3, Appli
c	33	18.2	58.7	720	3	US-08-333-840-3	Sequence 3, Appli
	34	18.2	58.7	972	3	US-10-668-047A-3	Sequence 3, Appli
	35	18.2	58.7	975	3	US-09-248-796A-5867	Sequence 5867, Ap
	36	18	58.1	4494	3	US-09-902-540-659	Sequence 659, App
c	37	17.8	57.4	530	3	US-09-533-559-2601	Sequence 2601, Ap
c	38	17.8	57.4	601	3	US-09-949-016-70199	Sequence 70199, A
	39	17.8	57.4	969	3	US-09-188-930-11	Sequence 11, Appl
	40	17.8	57.4	969	3	US-09-312-283C-11	Sequence 11, Appl
	41	17.8	57.4	2343	3	US-09-902-540-6683	Sequence 6683, Ap
	42	17.8	57.4	2730	3	US-09-489-039A-6744	Sequence 6744, Ap
c	43	17.8	57.4	3247	3	US-09-902-540-526	Sequence 526, App
c	44	17.8	57.4	9225	3	US-09-543-681A-1336	Sequence 1336, Ap
	45	17.8	57.4	50062	3	US-09-949-016-13809	Sequence 13809, A

ALIGNMENTS

RESULT 1
US-09-252-991A-15978/c
; Sequence 15978, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15978
; LENGTH: 1806
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15978

Query Match 63.9%; Score 19.8; DB 3; Length 1806;
Best Local Similarity 77.4%; Pred. No. 21;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

```
Qy          1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              |||||||||||||  |||| | |||  |||
Db        538 TTCGCCACCGGAAGCCGAGTTGGCGGCACTG 508
```

RESULT 2
US-09-252-991A-16301
; Sequence 16301, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

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; SEQ ID NO 16301
;   LENGTH: 2289
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16301

  Query Match             63.9%;  Score 19.8;  DB 3;  Length 2289;
  Best Local Similarity   77.4%;  Pred. No. 22;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              | ||||||||||||  |||| | |||  |||
Db       1992 TTCGCCACCGGAAGCCGAGTTGGCGGCACTG 2022


RESULT 3
US-08-454-098-5
; Sequence 5, Application US/08454098
; Patent No. 6103521
;  GENERAL INFORMATION:
;    APPLICANT:  CAPON, DANIEL J
;    APPLICANT:  SMITH, DOUGLAS H
;    APPLICANT:  TIAN, HUAN
;    APPLICANT:  WINSLOW, GENINE A
;    APPLICANT:  SIEKEVITZ, MIRIAM
;    TITLE OF INVENTION:  MULTISPECIFIC CHIMERIC RECEPTORS
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CELL GENESYS, INC.
;      STREET:  322 LAKESIDE DRIVE
;      CITY:  FOSTER CITY
;      STATE:  CALIFORNIA
;      COUNTRY:  US
;      ZIP:  94404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/454,098
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/384,033
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KRUPEN, KAREN I
;      REGISTRATION NUMBER:  34,647
;      REFERENCE/DOCKET NUMBER:  CELL 18
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 358-9600 x131
;      TELEFAX:  (415) 349-7392
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-454-098-5

  Query Match             63.2%;  Score 19.6;  DB 3;  Length 111;
  Best Local Similarity   84.6%;  Pred. No. 16;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 CGCCACCGGAAGTTGAGTAGACGGTG 28
              || || |||||| |||| ||||||||
Db         81 CGTCAGCGGAAGATGAGGAGACGGTG 106


RESULT 4
PCT-US96-01600-5
; Sequence 5, Application PC/TUS9601600
;  GENERAL INFORMATION:
;    APPLICANT:  Capon, Daniel J.
;    APPLICANT:  Smith, Douglas H.
;    APPLICANT:  Tian, Huan
;    APPLICANT:  Winslow, Genine A.
;    APPLICANT:  Siekevitz, Miriam
;    TITLE OF INVENTION:  Multispecific Chimeric Receptors
;    NUMBER OF SEQUENCES:  26
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US96/01600
;      FILING DATE:  06-FEB-1996
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7639-051-228
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  111 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US96-01600-5

  Query Match             63.2%;  Score 19.6;  DB 6;  Length 111;
  Best Local Similarity   84.6%;  Pred. No. 16;
  Matches   22;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 CGCCACCGGAAGTTGAGTAGACGGTG 28
              || || |||||| |||| ||||||||
Db         81 CGTCAGCGGAAGATGAGGAGACGGTG 106


RESULT 5
US-09-464-535-13/c
; Sequence 13, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
;  APPLICANT: Famodu, Omolayo O.
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT: Sakai, Hajime
;  APPLICANT: McGonigle, Brian
;  APPLICANT: Rafalski, J. Antoni
;  TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
;  FILE REFERENCE: BB1306 US NA
;  CURRENT APPLICATION NUMBER: US/09/464,535
;  CURRENT FILING DATE: 1999-12-15
;  EARLIER APPLICATION NUMBER: 60/112,555
;  EARLIER FILING DATE: 1998-12-16
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
;   LENGTH: 436
;   TYPE: DNA
;   ORGANISM: Triticum aestivum
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US-09-464-535-13

Query Match 61.3%; Score 19; DB 3; Length 436;
Best Local Similarity 81.5%; Pred. No. 39;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          5 CCACCGGAAGTTGAGTAGACGGTGCTG 31
              |||||||||||||||  |   |||| ||
Db        157 CCACCGGAAGTTGAGCACCAGGTGGTG 131
```

RESULT 6
US-09-318-786-36/c
; Sequence 36, Application US/09318786
; Patent No. 6472147
; GENERAL INFORMATION:
; APPLICANT: Janda, Kim D
; APPLICANT: Wirsching, Peter
; APPLICANT: Lerner, Richard A
; APPLICANT: Gao, Changshou
; TITLE OF INVENTION: METHODS FOR DISPLAY OF HETERODIMERIC PROTEINS ON
; TITLE OF INVENTION: FILAMENTOUS PHAGE USING pVII AND pIX, COMPOSITIONS,
; TITLE OF INVENTION: VECTORS AND COMBINATORIAL LIBRARIES
; FILE REFERENCE: TSR0305S
; CURRENT APPLICATION NUMBER: US/09/318,786
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: nucleotide
; OTHER INFORMATION: encoding fusion polypeptide
US-09-318-786-36

Query Match 61.3%; Score 19; DB 3; Length 490;
Best Local Similarity 81.5%; Pred. No. 40;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          2 CCGCCACCGGAAGTTGAGTAGACGGTG 28
              || ||||| ||| ||||| | ||||||
Db        371 CCACCACCAGAACTTGAGGAAACGGTG 345
```

RESULT 7
US-09-464-535-39/c
; Sequence 39, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 39
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-464-535-39

Query Match 61.3%; Score 19; DB 3; Length 600;
Best Local Similarity 81.5%; Pred. No. 41;
Matches 22; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy          5 CCACCGGAAGTTGAGTAGACGGTGCTG 31
              |||||||||||||||  |   |||| ||
Db        164 CCACCGGAAGTTGAGCACCAGGTGGTG 138
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RESULT 8
US-09-464-535-31/c
; Sequence 31, Application US/09464535
; Patent No. 6545200
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Sakai, Hajime
; APPLICANT: McGonigle, Brian
; APPLICANT: Rafalski, J. Antoni
; TITLE OF INVENTION: STEROL BIOSYNTHETIC ENZYMES
; FILE REFERENCE: BB1306 US NA
; CURRENT APPLICATION NUMBER: US/09/464,535
; CURRENT FILING DATE: 1999-12-15
; EARLIER APPLICATION NUMBER: 60/112,555
; EARLIER FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 31
; LENGTH: 673
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (41)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (95)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (227)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (385)
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; NAME/KEY: unsure
; LOCATION: (388)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (390)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (487)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (491)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (554)
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; NAME/KEY: unsure
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; LOCATION: (626)
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; NAME/KEY: unsure
; LOCATION: (634)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (650)

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;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (664)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (668)
US-09-464-535-31

  Query Match             61.3%;  Score 19;  DB 3;  Length 673;
  Best Local Similarity   81.5%;  Pred. No. 42;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          5 CCACCGGAAGTTGAGTAGACGGTGCTG 31
              ||||||||||||||| |   |||| ||
Db        362 CCACCGGAAGTTGAGCACCAGGTGGTG 336


RESULT 9
US-09-351-224E-7/c
; Sequence 7, Application US/09351224E
; Patent No. 6388171
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jon
;  APPLICANT:  Maddox, Joyce
;  APPLICANT:  Gilliam, Jacob
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Crasta, Oswald R.
;  TITLE OF INVENTION: Compositions and Methods for Fumonisin
;  TITLE OF INVENTION:  Detoxification
;  FILE REFERENCE: 5718-111
;  CURRENT APPLICATION NUMBER: US/09/351,224E
;  CURRENT FILING DATE:  1999-07-12
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 1578
;   TYPE: DNA
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: permease, fully spliced cDNA
US-09-351-224E-7

  Query Match             61.3%;  Score 19;  DB 3;  Length 1578;
  Best Local Similarity   81.5%;  Pred. No. 49;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 GCCACCGGAAGTTGAGTAGACGGTGCT 30
              |||||||| ||| | ||||||| || |
Db        321 GCCACCGGCAGTCGGGTAGACGCTGGT 295


RESULT 10
US-09-677-488A-7/c
; Sequence 7, Application US/09677488A
; Patent No. 6482621
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jon
;  APPLICANT:  Maddox, Joyce
;  APPLICANT:  Gilliam, Jacob
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Crasta, Oswald R.
;  TITLE OF INVENTION: Compositions and Methods for Fumonisin
;  TITLE OF INVENTION:  Detoxification
;  FILE REFERENCE: 35718/204100
;  CURRENT APPLICATION NUMBER: US/09/677,488A
;  CURRENT FILING DATE:  2000-10-02
;  PRIOR APPLICATION NUMBER: 09/351,224
;  PRIOR FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 1578
;   TYPE: DNA
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: permease, fully spliced cDNA
US-09-677-488A-7

  Query Match             61.3%;  Score 19;  DB 3;  Length 1578;
  Best Local Similarity   81.5%;  Pred. No. 49;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 GCCACCGGAAGTTGAGTAGACGGTGCT 30
              |||||||| ||| | ||||||| || |
Db        321 GCCACCGGCAGTCGGGTAGACGCTGGT 295


RESULT 11
US-09-677-682B-7/c
; Sequence 7, Application US/09677682B
; Patent No. 6534291
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jon
;  APPLICANT:  Maddox, Joyce
;  APPLICANT:  Gilliam, Jacob
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Crasta, Oswald R.
;  TITLE OF INVENTION: Compositions and Methods for Fumonisin
;  TITLE OF INVENTION:  Detoxification
;  FILE REFERENCE: 35718/204101
;  CURRENT APPLICATION NUMBER: US/09/677,682B
;  CURRENT FILING DATE:  2000-10-02
;  PRIOR APPLICATION NUMBER: 09/351,224
;  PRIOR FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 1578
;   TYPE: DNA
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: permease, fully spliced cDNA
US-09-677-682B-7

  Query Match             61.3%;  Score 19;  DB 3;  Length 1578;
  Best Local Similarity   81.5%;  Pred. No. 49;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 GCCACCGGAAGTTGAGTAGACGGTGCT 30
              |||||||| ||| | ||||||| || |
Db        321 GCCACCGGCAGTCGGGTAGACGCTGGT 295


RESULT 12
US-09-882-694B-7/c
; Sequence 7, Application US/09882694B
; Patent No. 6822140
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jon
;  APPLICANT:  Maddox, Joyce
;  APPLICANT:  Gilliam, Jacob
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Crasta, Oswald R.
;  TITLE OF INVENTION: Compositions and Methods for Fumonisin
;  TITLE OF INVENTION:  Detoxification
;  FILE REFERENCE: 35718/208255
;  CURRENT APPLICATION NUMBER: US/09/882,694B
;  CURRENT FILING DATE:  2001-06-15
;  PRIOR APPLICATION NUMBER: 09/351,224
;  PRIOR FILING DATE: 1999-07-12
```

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;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 1578
;   TYPE: DNA
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1578)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: permease, fully spliced cDNA
US-09-882-694B-7

  Query Match             61.3%;  Score 19;  DB 3;  Length 1578;
  Best Local Similarity   81.5%;  Pred. No. 49;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 GCCACCGGAAGTTGAGTAGACGGTGCT 30
              |||||||| ||| | ||||||| || |
Db        321 GCCACCGGCAGTCGGGTAGACGCTGGT 295


RESULT 13
US-09-351-224E-6/c
; Sequence 6, Application US/09351224E
; Patent No. 6388171
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jon
;  APPLICANT:  Maddox, Joyce
;  APPLICANT:  Gilliam, Jacob
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Crasta, Oswald R.
;  TITLE OF INVENTION: Compositions and Methods for Fumonisin
;  TITLE OF INVENTION:  Detoxification
;  FILE REFERENCE: 5718-111
;  CURRENT APPLICATION NUMBER: US/09/351,224E
;  CURRENT FILING DATE:  1999-07-12
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 1764
;   TYPE: DNA
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: permease, partially spliced cDNA
US-09-351-224E-6

  Query Match             61.3%;  Score 19;  DB 3;  Length 1764;
  Best Local Similarity   81.5%;  Pred. No. 50;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 GCCACCGGAAGTTGAGTAGACGGTGCT 30
              |||||||| ||| | ||||||| || |
Db        325 GCCACCGGCAGTCGGGTAGACGCTGGT 299


RESULT 14
US-09-677-488A-6/c
; Sequence 6, Application US/09677488A
; Patent No. 6482621
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jon
;  APPLICANT:  Maddox, Joyce
;  APPLICANT:  Gilliam, Jacob
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Crasta, Oswald R.
;  TITLE OF INVENTION: Compositions and Methods for Fumonisin
;  TITLE OF INVENTION:  Detoxification
;  FILE REFERENCE: 35718/204100
;  CURRENT APPLICATION NUMBER: US/09/677,488A
;  CURRENT FILING DATE:  2000-10-02
;  PRIOR APPLICATION NUMBER: 09/351,224
;  PRIOR FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 1764
;   TYPE: DNA
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: permease, partially spliced cDNA
US-09-677-488A-6

  Query Match             61.3%;  Score 19;  DB 3;  Length 1764;
  Best Local Similarity   81.5%;  Pred. No. 50;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 GCCACCGGAAGTTGAGTAGACGGTGCT 30
              |||||||| ||| | ||||||| || |
Db        325 GCCACCGGCAGTCGGGTAGACGCTGGT 299


RESULT 15
US-09-677-682B-6/c
; Sequence 6, Application US/09677682B
; Patent No. 6534291
; GENERAL INFORMATION:
;  APPLICANT: Duvick, Jon
;  APPLICANT:  Maddox, Joyce
;  APPLICANT:  Gilliam, Jacob
;  APPLICANT:  Folkerts, Otto
;  APPLICANT:  Crasta, Oswald R.
;  TITLE OF INVENTION: Compositions and Methods for Fumonisin
;  TITLE OF INVENTION:  Detoxification
;  FILE REFERENCE: 35718/204101
;  CURRENT APPLICATION NUMBER: US/09/677,682B
;  CURRENT FILING DATE:  2000-10-02
;  PRIOR APPLICATION NUMBER: 09/351,224
;  PRIOR FILING DATE: 1999-07-12
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 1764
;   TYPE: DNA
;   ORGANISM: Exophiala spinifera
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: permease, partially spliced cDNA
US-09-677-682B-6

  Query Match             61.3%;  Score 19;  DB 3;  Length 1764;
  Best Local Similarity   81.5%;  Pred. No. 50;
  Matches   22;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 GCCACCGGAAGTTGAGTAGACGGTGCT 30
              |||||||| ||| | ||||||| || |
Db        325 GCCACCGGCAGTCGGGTAGACGCTGGT 299


Search completed: December 12, 2005, 00:33:36
Job time : 82.1636 secs
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 00:28:08 ; Search time 393.418 Seconds
(without alignments)
651.599 Million cell updates/sec

Title: US-10-688-489-59
Perfect score: 31
Sequence: 1 tccgccaccggaagttgagtagacggtgctg 31

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	31	100.0	31	8	US-10-688-489-59	Sequence 59, Appl
2	30	96.8	10945	7	US-10-361-002-5	Sequence 5, Appli
3	30	96.8	10945	7	US-10-361-004-5	Sequence 5, Appli
4	30	96.8	10975	8	US-10-699-550-1	Sequence 1, Appli
5	30	96.8	11029	8	US-10-699-550-2	Sequence 2, Appli
6	30	96.8	11029	8	US-10-679-520A-66	Sequence 66, Appl
7	30	96.8	11029	9	US-10-706-892-1	Sequence 1, Appli
8	30	96.8	11029	9	US-10-706-892-2	Sequence 2, Appli
9	30	96.8	11029	9	US-10-985-805-1	Sequence 1, Appli
10	30	96.8	11029	9	US-10-956-085-1	Sequence 1, Appli
11	22	71.0	22	8	US-10-688-489-68	Sequence 68, Appl
12	21	67.7	21	8	US-10-688-489-63	Sequence 63, Appl
13	21	67.7	21	8	US-10-688-489-67	Sequence 67, Appl
14	21	67.7	21	8	US-10-688-489-70	Sequence 70, Appl
15	20.6	66.5	21	10	US-11-110-517-1	Sequence 1, Appli
16	20.6	66.5	43	5	US-10-196-793A-32	Sequence 32, Appl
17	20.6	66.5	590	4	US-09-925-065A-446157	Sequence 446157,
18	20.6	66.5	590	4	US-09-925-065A-446158	Sequence 446158,
c 19	20.6	66.5	1500	9	US-10-964-195-12	Sequence 12, Appl
c 20	20.6	66.5	1517	9	US-10-964-195-10	Sequence 10, Appl
c 21	20.6	66.5	1527	6	US-10-074-596-10	Sequence 10, Appl
22	20.4	65.8	612	4	US-09-925-065A-854826	Sequence 854826,
23	20	64.5	20	8	US-10-688-489-62	Sequence 62, Appl
24	20	64.5	20	8	US-10-688-489-69	Sequence 69, Appl
25	20	64.5	20	8	US-10-688-489-71	Sequence 71, Appl
26	20	64.5	20	9	US-10-985-805-52	Sequence 52, Appl
27	20	64.5	342	8	US-10-815-480-30	Sequence 30, Appl
28	20	64.5	342	8	US-10-815-480-32	Sequence 32, Appl
29	20	64.5	411	8	US-10-815-480-38	Sequence 38, Appl
30	20	64.5	418	8	US-10-815-480-29	Sequence 29, Appl
31	20	64.5	418	8	US-10-815-480-31	Sequence 31, Appl
32	20	64.5	418	8	US-10-815-480-33	Sequence 33, Appl
33	20	64.5	418	8	US-10-815-480-34	Sequence 34, Appl
34	20	64.5	418	8	US-10-815-480-35	Sequence 35, Appl
35	19.8	63.9	1104	9	US-10-450-763-9300	Sequence 9300, Ap
c 36	19.8	63.9	1149	7	US-10-282-122A-6914	Sequence 6914, Ap
37	19.8	63.9	1479	7	US-10-282-122A-7527	Sequence 7527, Ap
c 38	19.8	63.9	2149	5	US-10-027-632-103171	Sequence 103171,
c 39	19.8	63.9	2149	5	US-10-027-632-103172	Sequence 103172,
c 40	19.8	63.9	2149	6	US-10-027-632-103171	Sequence 103171,
c 41	19.8	63.9	2149	6	US-10-027-632-103172	Sequence 103172,
42	19.8	63.9	2878	7	US-10-600-230-69	Sequence 69, Appl
c 43	19.8	63.9	5931	10	US-11-097-143-35048	Sequence 35048, A
44	19.8	63.9	7931	10	US-11-097-143-35047	Sequence 35047, A
c 45	19.6	63.2	517	4	US-09-925-065A-356395	Sequence 356395,

ALIGNMENTS

RESULT 1
US-10-688-489-59
; Sequence 59, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 31
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-59

Query Match 100.0%; Score 31; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              |||||||||||||||||||||||||||||||
Db          1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
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RESULT 2
US-10-361-002-5
; Sequence 5, Application US/10361002
; Publication No. US20040170954A1
; GENERAL INFORMATION:
; APPLICANT: Clearant, Inc.
; APPLICANT: McKenney, Keith
; APPLICANT: Gillmeister, Lidja

```
;  APPLICANT:  Marlowe, Kristina
;  APPLICANT:  Armistead, David
;  TITLE OF INVENTION: Pathogen Inactivation Assay
;  FILE REFERENCE: CI-0043
;  CURRENT APPLICATION NUMBER: US/10/361,002
;  CURRENT FILING DATE:  2003-02-10
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 10945
;   TYPE: DNA
;   ORGANISM: West Nile virus
US-10-361-002-5

  Query Match             96.8%;  Score 30;  DB 7;  Length 10945;
  Best Local Similarity   100.0%;  Pred. No. 0.00094;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              ||||||||||||||||||||||||||||||
Db      10481 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10510


RESULT 3
US-10-361-004-5
; Sequence 5, Application US/10361004
; Publication No. US20040170981A1
; GENERAL INFORMATION:
;  APPLICANT: Clearant, Inc.
;  APPLICANT:  McKenney, Keith
;  APPLICANT:  Gillmeister, Lidja
;  APPLICANT:  Marlowe, Kristina
;  APPLICANT:  Armistad, David
;  TITLE OF INVENTION: Real-Time Polymerase Chain Reaction Using Large Target Amplicons
;  FILE REFERENCE: CI-0042
;  CURRENT APPLICATION NUMBER: US/10/361,004
;  CURRENT FILING DATE:  2003-02-10
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 10945
;   TYPE: DNA
;   ORGANISM: West Nile virus
US-10-361-004-5

  Query Match             96.8%;  Score 30;  DB 7;  Length 10945;
  Best Local Similarity   100.0%;  Pred. No. 0.00094;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              ||||||||||||||||||||||||||||||
Db      10481 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10510


RESULT 4
US-10-699-550-1
; Sequence 1, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
;  APPLICANT: WONG, SUSAN J.
;  APPLICANT:  SHI, PEI-YONG
;  TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
;  FILE REFERENCE: 454311-2232.1
;  CURRENT APPLICATION NUMBER: US/10/699,550
;  CURRENT FILING DATE:  2003-10-31
;  PRIOR APPLICATION NUMBER: 60/476,513
;  PRIOR FILING DATE: 2003-06-06
;  PRIOR APPLICATION NUMBER: 60/422,755
;  PRIOR FILING DATE: 2002-10-31
;  PRIOR APPLICATION NUMBER: PCT/US02/09036
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: 60/402,860
;  PRIOR FILING DATE: 20Q2-08-08
;  PRIOR APPLICATION NUMBER: 60/281,947
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/275,025
;  PRIOR FILING DATE: 2001-03-12
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
;   LENGTH: 10975
;   TYPE: DNA
;   ORGANISM: West Nile virus
US-10-699-550-1

  Query Match             96.8%;  Score 30;  DB 8;  Length 10975;
  Best Local Similarity   100.0%;  Pred. No. 0.00094;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              ||||||||||||||||||||||||||||||
Db      10505 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10534


RESULT 5
US-10-699-550-2
; Sequence 2, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
;  APPLICANT: WONG, SUSAN J.
;  APPLICANT:  SHI, PEI-YONG
;  TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
;  FILE REFERENCE: 454311-2232.1
;  CURRENT APPLICATION NUMBER: US/10/699,550
;  CURRENT FILING DATE:  2003-10-31
;  PRIOR APPLICATION NUMBER: 60/476,513
;  PRIOR FILING DATE: 2003-06-06
;  PRIOR APPLICATION NUMBER: 60/422,755
;  PRIOR FILING DATE: 2002-10-31
;  PRIOR APPLICATION NUMBER: PCT/US02/09036
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: 60/402,860
;  PRIOR FILING DATE: 2002-08-08
;  PRIOR APPLICATION NUMBER: 60/281,947
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/275,025
;  PRIOR FILING DATE: 2001-03-12
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
;   LENGTH: 11029
;   TYPE: DNA
;   ORGANISM: West Nile virus
US-10-699-550-2

  Query Match             96.8%;  Score 30;  DB 8;  Length 11029;
  Best Local Similarity   100.0%;  Pred. No. 0.00094;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              ||||||||||||||||||||||||||||||
Db      10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552


RESULT 6
US-10-679-520A-66
; Sequence 66, Application US/10679520A
; Publication No. US20050031641A1
; GENERAL INFORMATION:
;  APPLICANT: LOOSMORE, SHEENA MAY
;  APPLICANT:  AUDONNET, JEAN-CHRISTOPHE FRANCIS
;  APPLICANT:  MINKE, JULES MAARTEN
;  TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
;  FILE REFERENCE: 574313-3161.4
;  CURRENT APPLICATION NUMBER: US/10/679,520A
;  CURRENT FILING DATE:  2003-10-06
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;  PRIOR APPLICATION NUMBER: 10/374,953
;  PRIOR FILING DATE: 2003-02-26
;  PRIOR APPLICATION NUMBER: 10/116,298
;  PRIOR FILING DATE: 2002-04-04
;  PRIOR APPLICATION NUMBER: 60/281,923
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: PCT/FR02/01200
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: FR 01/04737
;  PRIOR FILING DATE: 2001-04-06
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
;   LENGTH: 11029
;   TYPE: DNA
;   ORGANISM: West Nile virus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (97)..(10395)
US-10-679-520A-66

  Query Match             96.8%;  Score 30;  DB 8;  Length 11029;
  Best Local Similarity   100.0%;  Pred. No. 0.00094;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              ||||||||||||||||||||||||||||||
Db      10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552


RESULT 7
US-10-706-892-1
; Sequence 1, Application US/10706892
; Publication No. US20050058987A1
; GENERAL INFORMATION:
;  APPLICANT: SHI, PEI-YONG
;  TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY
;  FILE REFERENCE: 454311-2231.1
;  CURRENT APPLICATION NUMBER: US/10/706,892
;  CURRENT FILING DATE:  2003-11-13
;  PRIOR APPLICATION NUMBER: 60/427,117
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
;   LENGTH: 11029
;   TYPE: DNA
;   ORGANISM: West Nile virus
US-10-706-892-1

  Query Match             96.8%;  Score 30;  DB 9;  Length 11029;
  Best Local Similarity   100.0%;  Pred. No. 0.00094;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              ||||||||||||||||||||||||||||||
Db      10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552


RESULT 8
US-10-706-892-2
; Sequence 2, Application US/10706892
; Publication No. US20050058987A1
; GENERAL INFORMATION:
;  APPLICANT: SHI, PEI-YONG
;  TITLE OF INVENTION: SCREENING FOR WEST NILE VIRUS ANTIVIRAL THERAPY
;  FILE REFERENCE: 454311-2231.1
;  CURRENT APPLICATION NUMBER: US/10/706,892
;  CURRENT FILING DATE:  2003-11-13
;  PRIOR APPLICATION NUMBER: 60/427,117
;  PRIOR FILING DATE: 2002-11-18
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
;   LENGTH: 11029
;   TYPE: DNA
;   ORGANISM: West Nile virus
US-10-706-892-2

  Query Match             96.8%;  Score 30;  DB 9;  Length 11029;
  Best Local Similarity   100.0%;  Pred. No. 0.00094;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              ||||||||||||||||||||||||||||||
Db      10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552


RESULT 9
US-10-985-805-1
; Sequence 1, Application US/10985805
; Publication No. US20050130133A1
; GENERAL INFORMATION:
;  APPLICANT: Burde, Stefan H.M.
;  APPLICANT:  Gierman, Todd M.
;  APPLICANT:  Glenn, Christopher C.
;  TITLE OF INVENTION: Oligonucleotides and Methods for Detection of West Nile Virus
;  FILE REFERENCE: 7430*201
;  CURRENT APPLICATION NUMBER: US/10/985,805
;  CURRENT FILING DATE:  2004-11-10
;  PRIOR APPLICATION NUMBER: US 60/519,096
;  PRIOR FILING DATE: 2003-11-12
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 11029
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: West Nile virus consensus sequence
US-10-985-805-1

  Query Match             96.8%;  Score 30;  DB 9;  Length 11029;
  Best Local Similarity   100.0%;  Pred. No. 0.00094;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              ||||||||||||||||||||||||||||||
Db      10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552


RESULT 10
US-10-956-085-1
; Sequence 1, Application US/10956085
; Publication No. US20050164170A1
; GENERAL INFORMATION:
;  APPLICANT: DESPRES, PHILIPPE
;  APPLICANT:  DEUBEL, VINCENT
;  APPLICANT:  GUENET, JEAN-LOUIS
;  APPLICANT:  DROUET, MARIE-THERESE
;  APPLICANT:  MALKINSON, MERTYN
;  APPLICANT:  BANET, CAROLINE
;  APPLICANT:  FRENKIEL, MARIE-PASCALE
;  APPLICANT:  COURAGEOT, MARIE-PIERRE
;  APPLICANT:  COULIBALY, FASSELI
;  APPLICANT:  CATTEAU, ADELINE
;  APPLICANT:  FLAMAND, MARIE
;  TITLE OF INVENTION: NEUROVIRULENT STRAIN OF THE WEST NILE VIRUS AND APPLICATIONS
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 243477US0XPCT
;  CURRENT APPLICATION NUMBER: US/10/956,085
;  CURRENT FILING DATE:  2004-10-04
;  PRIOR APPLICATION NUMBER: PCT/FR02/01168
;  PRIOR FILING DATE: 2002-04-04
;  PRIOR APPLICATION NUMBER: FR01/04599
;  PRIOR FILING DATE: 2001-04-04
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;  PRIOR APPLICATION NUMBER: FR01/11525
;  PRIOR FILING DATE: 2001-09-06
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
;   LENGTH: 11029
;   TYPE: DNA
;   ORGANISM: Flavivirus sp.
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (97)..(10395)
US-10-956-085-1

  Query Match            96.8%;  Score 30;  DB 9;  Length 11029;
  Best Local Similarity  100.0%;  Pred. No. 0.00094;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              ||||||||||||||||||||||||||||||
Db      10523 CCGCCACCGGAAGTTGAGTAGACGGTGCTG 10552


RESULT 11
US-10-688-489-68
; Sequence 68, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 68
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-68

  Query Match            71.0%;  Score 22;  DB 8;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 3.5;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGAAGTTGAGTAGACGGTGCTG 31
              ||||||||||||||||||||||
Db          1 GGAAGTTGAGTAGACGGTGCTG 22


RESULT 12
US-10-688-489-63
; Sequence 63, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-63

  Query Match            67.7%;  Score 21;  DB 8;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 10;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGCCACCGGAAGTTGAGTA 21
              |||||||||||||||||||||
Db          1 TCCGCCACCGGAAGTTGAGTA 21


RESULT 13
US-10-688-489-67
; Sequence 67, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 67
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-67

  Query Match            67.7%;  Score 21;  DB 8;  Length 21;
  Best Local Similarity  100.0%;  Pred. No. 10;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGAAGTTGAGTAGACGGTGCT 30
              |||||||||||||||||||||
Db          1 GGAAGTTGAGTAGACGGTGCT 21


RESULT 14
US-10-688-489-70
; Sequence 70, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
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;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 70
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-70

  Query Match             67.7%;  Score 21;  DB 8;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 10;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GAAGTTGAGTAGACGGTGCTG 31
              |||||||||||||||||||||
Db          1 GAAGTTGAGTAGACGGTGCTG 21


RESULT 15
US-11-110-517-1
; Sequence 1, Application US/11110517
; Publication No. US20050186222A1
; GENERAL INFORMATION:
;  APPLICANT: Crucell Holland B.V.
;  APPLICANT:  UytdeHaag, Alphonsus GCM
;  APPLICANT:  Goudsmit, Jaap
;  APPLICANT:  Schouten, Govert J
;  TITLE OF INVENTION: Vaccine against West Nile virus
;  FILE REFERENCE: 0082WO00ORD
;  CURRENT APPLICATION NUMBER: US/11/110,517
;  CURRENT FILING DATE:  2005-04-20
;  PRIOR APPLICATION NUMBER: PCT/NL02/00718
;  PRIOR FILING DATE: 2002-11-08
;  PRIOR APPLICATION NUMBER: PCT/EP03/50129
;  PRIOR FILING DATE: 2003-04-28
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic oligonucleotide WNV 1
US-11-110-517-1

  Query Match             66.5%;  Score 20.6;  DB 10;  Length 21;
  Best Local Similarity   95.2%;  Pred. No. 16;
  Matches   20;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 CCACCGGAAGTTGAGTAGACG 25
              ||||||||:||||||||||||
Db          1 CCACCGGAWGTTGAGTAGACG 21


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GenCore version 5.1.6

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(without alignments)
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Perfect score: 31
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1209584

Minimum DB seq length: 18
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Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	12	38.7	20	6	AX045081	AX045081 Sequence
	2	12	38.7	20	6	AX350865	AX350865 Sequence
	3	12	38.7	21	6	CQ815914	CQ815914 Sequence
c	4	11	35.5	19	6	AX429360	AX429360 Sequence
c	5	11	35.5	20	6	BD089943	BD089943 A method
c	6	11	35.5	21	6	CS014127	CS014127 Sequence
	7	11	35.5	21	6	AX676187	AX676187 Sequence
c	8	11	35.5	22	6	AR649551	AR649551 Sequence
c	9	11	35.5	23	6	BD176902	BD176902 Gene enco
c	10	11	35.5	23	6	BD266802	BD266802 Methods f
c	11	11	35.5	23	6	AX587376	AX587376 Sequence
c	12	11	35.5	24	6	E07234	E07234 Primer. 9/1
c	13	11	35.5	24	6	I32494	I32494 Sequence 14
c	14	11	35.5	24	6	I43439	I43439 Sequence 14
c	15	11	35.5	24	6	AR181929	AR181929 Sequence
c	16	11	35.5	24	6	AR494625	AR494625 Sequence
c	17	11	35.5	24	6	AR656106	AR656106 Sequence
	18	11	35.5	24	6	AX445342	AX445342 Sequence
	19	11	35.5	24	6	AX494089	AX494089 Sequence
	20	11	35.5	25	6	AR137232	AR137232 Sequence
	21	11	35.5	25	6	AR156944	AR156944 Sequence
c	22	11	35.5	25	6	AR350223	AR350223 Sequence
c	23	11	35.5	25	6	AX354290	AX354290 Sequence
c	24	11	35.5	29	6	AX192031	AX192031 Sequence
c	25	11	35.5	31	6	AR656122	AR656122 Sequence
c	26	11	35.5	31	6	AR656136	AR656136 Sequence
	27	10	32.3	18	6	BD074284	BD074284 Method fo
	28	10	32.3	18	6	BD128481	BD128481 EF-Tu mRN
	29	10	32.3	18	6	E35345	E35345 Assay for m
c	30	10	32.3	18	6	E44089	E44089 Primer for
	31	10	32.3	18	6	AR258037	AR258037 Sequence
	32	10	32.3	18	6	AR428497	AR428497 Sequence
	33	10	32.3	18	6	AR489881	AR489881 Sequence
	34	10	32.3	18	6	AX004854	AX004854 Sequence
	35	10	32.3	18	6	AX019826	AX019826 Sequence
	36	10	32.3	18	6	BD017760	BD017760 Test for
	37	10	32.3	19	6	A33825	A33825 Synthetic p
	38	10	32.3	19	6	AR083883	AR083883 Sequence
c	39	10	32.3	19	6	CQ787542	CQ787542 Sequence
c	40	10	32.3	19	6	CQ807359	CQ807359 Sequence
	41	10	32.3	19	6	CQ807675	CQ807675 Sequence
	42	10	32.3	19	6	CQ987507	CQ987507 Sequence
c	43	10	32.3	19	6	CQ987832	CQ987832 Sequence
	44	10	32.3	19	6	E06911	E06911 Synthetic D
	45	10	32.3	19	6	I27509	I27509 Sequence 23

ALIGNMENTS

RESULT 1
AX045081/c
LOCUS AX045081 20 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 11 from Patent WO0066149.
ACCESSION AX045081
VERSION AX045081.1 GI:11343680
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1
AUTHORS Gerhardt,C., Romero-Romero,I.A. and Strosberg,A.D.
TITLE Medicines useful for treating disorders of regulation of body fatness and diseases related to disorders of leptin production
JOURNAL Patent: WO 0066149-A 11 09-NOV-2000;
CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (FR)
FEATURES Location/Qualifiers
source 1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="AMORCE"
ORIGIN

Query Match 38.7%; Score 12; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 TGAGTAGACGGT 27
||||||||||||
Db 18 TGAGTAGACGGT 7

RESULT 2
AX350865
LOCUS AX350865 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 5 from Patent WO0183816.
ACCESSION AX350865
VERSION AX350865.1 GI:18616322
KEYWORDS .
SOURCE synthetic construct

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  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Neri,D. and Viti,F.
  TITLE     Method for detecting tumors
  JOURNAL   Patent: WO 0183816-A 5 08-NOV-2001;
            Philogen S.R.L. (IT)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
ORIGIN

  Query Match             38.7%;  Score 12;  DB 6;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 3.7e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 ACCGGAAGTTGA 18
              ||||||||||||
Db          7 ACCGGAAGTTGA 18


RESULT 3
CQ815914
LOCUS       CQ815914                  21 bp    DNA     linear   PAT 03-JUN-2004
DEFINITION  Sequence 1 from Patent WO2004042042.
ACCESSION   CQ815914
VERSION     CQ815914.1  GI:48144439
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Uytdehaag,A.G., Schouten,G.J. and Goudsmit,J.
  TITLE     Vaccines against west nile virus
  JOURNAL   Patent: WO 2004042042-A 1 21-MAY-2004;
            Crucell Holland B.V. (NL)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Synthetic oligonucleotide WNV 1"
ORIGIN

  Query Match             38.7%;  Score 12;  DB 6;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.8e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 GTTGAGTAGACG 25
              ||||||||||||
Db         10 GTTGAGTAGACG 21


RESULT 4
AX429360/c
LOCUS       AX429360                  19 bp    DNA     linear   PAT 21-JUN-2002
DEFINITION  Sequence 6 from Patent WO0234953.
ACCESSION   AX429360
VERSION     AX429360.1  GI:21540661
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Reynolds,T.R.
  TITLE     Detection and quantification of human herpes viruses
  JOURNAL   Patent: WO 0234953-A 6 02-MAY-2002;
            HARRIS, ROBERT B (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Probe"
ORIGIN

  Query Match             35.5%;  Score 11;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 AGACGGTGCTG 31
              ||||||||||||
Db         16 AGACGGTGCTG 6


RESULT 5
BD089943/c
LOCUS       BD089943                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD089943
VERSION     BD089943.1  GI:22635553
KEYWORDS    JP 2001321190-A/2187.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 2187 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/2187
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 ACCGGAAGTTG 17
              ||||||||||||
Db         19 ACCGGAAGTTG 9


RESULT 6
CS014127/c
LOCUS       CS014127                  21 bp    DNA     linear   PAT 11-FEB-2005
DEFINITION  Sequence 4052 from Patent WO2005007144.
ACCESSION   CS014127
VERSION     CS014127.1  GI:59673942
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hakonarson,H., Gurney,M.E. and Halapi,E.
```

```
  TITLE     Methods of diagnosis and treatment for asthma based on haplotype
            association
  JOURNAL   Patent: WO 2005007144-A 4052 27-JAN-2005;
            Decode Genetics EHF. (IS)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           35.5%;  Score 11;  DB 6;  Length 21;
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  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GAAGTTGAGTA 21
               ||||||||||
Db         19 GAAGTTGAGTA 9


RESULT 7
AX676187
LOCUS       AX676187                 21 bp    DNA     linear   PAT 27-MAR-2003
DEFINITION  Sequence 44 from Patent WO02057429.
ACCESSION   AX676187
VERSION     AX676187.1  GI:29333863
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Yan,W.L.
  TITLE     A method for producing a population of homozygous stem cells having
            a pre-selected immunophenotype and/or genotype
  JOURNAL   Patent: WO 02057429-A 44 25-JUL-2002;
            Stemron, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer"
ORIGIN

  Query Match           35.5%;  Score 11;  DB 6;  Length 21;
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  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GAAGTTGAGTA 21
               ||||||||||
Db          4 GAAGTTGAGTA 14


RESULT 8
AR649551/c
LOCUS       AR649551                 22 bp    DNA     linear   PAT 20-APR-2005
DEFINITION  Sequence 20 from patent US 6875757.
ACCESSION   AR649551
VERSION     AR649551.1  GI:62792791
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Miller,D.D., Tigyi,G., Dalton,J.T., Sardar,V.M., Elrod,D.B., Xu,H.,
            Baker,D.L., Wang,D., Liliom,K., Fischer,D.J., Virag,T. and
            Nusser,N.
  TITLE     LPA receptor agonists and antagonists and methods of use
  JOURNAL   Patent: US 6875757-A 20 05-APR-2005;
            University of Tennessee Research Foundation; Knoxville, TN
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           35.5%;  Score 11;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 AGACGGTGCTG 31
               ||||||||||
Db         17 AGACGGTGCTG 7


RESULT 9
BD176902/c
LOCUS       BD176902                 23 bp    DNA     linear   PAT 18-MAR-2003
DEFINITION  Gene encoding an amino acid sequence relating to cytokinin
            synthesis.
ACCESSION   BD176902
VERSION     BD176902.1  GI:29122830
KEYWORDS    WO 02072818-A/22.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Kakimoto,T. and Sakakibara,H.
  TITLE     Gene encoding an amino acid sequence relating to cytokinin
            synthesis
  JOURNAL   Patent: WO 02072818-A 22 19-SEP-2002;
            SUNTORY LTD,NIPPON PAPER INDUSTRIES CO LTD,TATSUO KAKIMOTO, HITOSHI
            SAKAKIBARA
COMMENT     OS   Artificial Sequence
            PN   WO 02072818-A/22
            PD   19-SEP-2002
            PF   12-MAR-2002 WO 2002JP002315
            PR   12-MAR-2001 JP 01P   069489
            PI   TATSUO KAKIMOTO,HITOSHI SAKAKIBARA
            PC   C12N15/09,C12N5/14,C12N9/10,C12Q1/68,A01H5/00 CC   Primer 918
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match           35.5%;  Score 11;  DB 6;  Length 23;
  Best Local Similarity  100.0%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGAAGTTGAGT 20
               ||||||||||
Db         19 GGAAGTTGAGT 9


RESULT 10
BD266802/c
LOCUS       BD266802                 23 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Methods for treating cancer and for mediating chemotaxis of
            dendritic cells.
ACCESSION   BD266802
VERSION     BD266802.1  GI:33076570
KEYWORDS    JP 2002533402-A/22.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Keting,C., Xin,H., Chan,V.W.F., Kothakota,S., Williams,L.T. and
            Winter,J.A.
  TITLE     Methods for treating cancer and for mediating chemotaxis of
            dendritic cells
  JOURNAL   Patent: JP 2002533402-A 22 08-OCT-2002;
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            CHIRON CORP
COMMENT     OS   Artificial Sequence
            PN   JP 2002533402-A/22
            PD   08-OCT-2002
            PF   28-DEC-1999 JP 2000590657
            PR   31-DEC-1998 US    60/114498
            PI   CHU KETING,HONG XIN,VIVIEN W F CHAN,SRINIVAS
            KOTHAKOTA,LEWIS T
            PI   WILLIAMS,
            PI   JILL A WINTER
            PC
            A61K38/00,A61K31/711,A61K39/395,A61K39/395,A61K45/00,A61K48/00, PC
             A61P35/00,
            PC   A61P37/00,A61P43/00,C07K14/47//C12N15/02,A61K37/02,C12N15/00
            CC   PCR Primer
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 GAGTAGACGGT 27
              ||||||||||
Db         23 GAGTAGACGGT 13


RESULT 11
AX587376/c
LOCUS       AX587376                  23 bp    DNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 152 from Patent WO0236761.
ACCESSION   AX587376
VERSION     AX587376.1  GI:27656241
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   D'Andrea,A.D., Taniguchi,T., Timmers,C. and Grompe,M.
  TITLE     Methods and compositions for the diagnosis of cancer
            susceptibilities and defective dna repair mechanisms and treatment
            thereof
  JOURNAL   Patent: WO 0236761-A 152 10-MAY-2002;
            DANA FARBER CANCER INSTITUTE (US)
FEATURES              Location/Qualifiers
     source           1. .23
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                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="MG758"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGAAGTTGAGT 20
              ||||||||||
Db         13 GGAAGTTGAGT 3


RESULT 12
E07234/c
LOCUS       E07234                    24 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  Primer.
ACCESSION   E07234
VERSION     E07234.1  GI:2175375
KEYWORDS    JP 1994100594-A/10.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Okuno,Y., Isekawa,Y., Sasao,F. and Ueda,S.
  TITLE     ANTI-HUMAN INFLUENZAL VIRUS ANTIBODY
  JOURNAL   Patent: JP 1994100594-A 10 12-APR-1994;
            TAKARA SHUZO CO LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1994100594-A/10
            PD   12-APR-1994
            PF   17-SEP-1992 JP 1992272538
            PI   OKUNO YOSHINOBU, ISEKAWA YUJI, SASAO FUYOKO, UEDA SHIGEHARU PC
              C07K13/00,A61K39/00,A61K39/00,A61K39/395,A61K39/395,C12N15/44, PC
              C12P21/02,
            PC
            C12P21/08,G01N33/53,G01N33/569,(C12P21/02,C12R1:91),(C12P21/08, PC
             C12R1:91);
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .24
            FT                   /organism='Artificial sequences'.
FEATURES              Location/Qualifiers
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                      /db_xref="taxon:32644"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AGTTGAGTAGA 23
              ||||||||||
Db         12 AGTTGAGTAGA 2


RESULT 13
I32494/c
LOCUS       I32494                    24 bp    DNA     linear   PAT 06-FEB-1997
DEFINITION  Sequence 14 from patent US 5589174.
ACCESSION   I32494
VERSION     I32494.1  GI:1823285
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.
  TITLE     Anti-human influenza virus antibody
  JOURNAL   Patent: US 5589174-A 14 31-DEC-1996;
FEATURES              Location/Qualifiers
     source           1. .24
                      /organism="unknown"
                      /mol_type="unassigned DNA"
ORIGIN

  Query Match             35.5%;  Score 11;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AGTTGAGTAGA 23
              ||||||||||
Db         12 AGTTGAGTAGA 2


RESULT 14
```

```
I43439/c
LOCUS       I43439                    24 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 14 from patent US 5631350.
ACCESSION   I43439
VERSION     I43439.1  GI:2468683
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.
  TITLE     Anti-human influenza virus antibody
  JOURNAL   Patent: US 5631350-A 14 20-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
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ORIGIN

  Query Match             35.5%;  Score 11;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AGTTGAGTAGA 23
              ||||||||||
Db         12 AGTTGAGTAGA 2


RESULT 15
AR181929/c
LOCUS       AR181929                  24 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 14 from patent US 6337070.
ACCESSION   AR181929
VERSION     AR181929.1  GI:20224845
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Okuno,Y., Isegawa,Y., Sasao,F. and Ueda,S.
  TITLE     Polypeptides for use in generating anti-human influenza virus
            antibodies
  JOURNAL   Patent: US 6337070-A 14 08-JAN-2002;
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             35.5%;  Score 11;  DB 6;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AGTTGAGTAGA 23
              ||||||||||
Db         12 AGTTGAGTAGA 2


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GenCore version 5.1.6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	31	100.0	31	12	ADN36737	Adn36737 West Nile
	2	22	71.0	22	12	ADN36746	Adn36746 West Nile
	3	21	67.7	21	12	ADN36741	Adn36741 West Nile
	4	21	67.7	21	12	ADN36745	Adn36745 West Nile
	5	21	67.7	21	12	ADN36748	Adn36748 West Nile
	6	20	64.5	20	12	ADN36749	Adn36749 West Nile
	7	20	64.5	20	12	ADN36740	Adn36740 West Nile
	8	20	64.5	20	12	ADN36747	Adn36747 West Nile
	9	20	64.5	20	14	AEA35007	Aea35007 West Nile
	10	19	61.3	19	12	ADN36744	Adn36744 West Nile
	11	19	61.3	19	12	ADN36738	Adn36738 West Nile
	12	18	58.1	18	12	ADN36742	Adn36742 West Nile
	13	18	58.1	19	12	ADN36739	Adn36739 West Nile
c	14	18	58.1	26	12	ADN36825	Adn36825 West Nile
	15	17	54.8	18	12	ADN36743	Adn36743 West Nile
	16	15	48.4	21	12	ADN36782	Adn36782 West Nile
	17	15	48.4	22	12	ADN36863	Adn36863 West Nile
	18	15	48.4	25	9	ACI27596	Aci27596 Human mic
	19	15	48.4	28	12	ADN36864	Adn36864 West Nile
c	20	13	41.9	18	2	AAV44610	Aav44610 Human unc
	21	13	41.9	19	12	ADN36783	Adn36783 West Nile
c	22	13	41.9	21	13	ADU29125	Adu29125 Knock-dow
	23	13	41.9	21	14	ADW91784	Adw91784 Phloem sm
	24	12	38.7	18	12	ADN36856	Adn36856 West Nile
	25	12	38.7	18	12	ADN36859	Adn36859 West Nile
	26	12	38.7	20	2	AAQ23778	Aaq23778 Herpesvir
c	27	12	38.7	20	4	AAC84110	Aac84110 Human alp
	28	12	38.7	20	6	ABL55945	Abl55945 Tumour de
	29	12	38.7	21	12	ADO21519	Ado21519 West Nile
c	30	12	38.7	24	6	ABZ70744	Abz70744 Human mac
c	31	12	38.7	25	9	ACI84612	Aci84612 Human mic
c	32	12	38.7	25	9	ACK01316	Ack01316 Human mic
	33	12	38.7	25	9	ACI48229	Aci48229 Human mic
c	34	12	38.7	25	9	ACI84613	Aci84613 Human mic
	35	12	38.7	25	9	ACK30551	Ack30551 Human mic
	36	12	38.7	25	9	ACI55477	Aci55477 Human mic
	37	12	38.7	26	13	ADZ17390	Adz17390 Mutagenic
c	38	11	35.5	18	14	AEB09625	Aeb09625 Human sph
c	39	11	35.5	19	6	ABK86406	Abk86406 HSV2 thym
c	40	11	35.5	19	6	ABA01459	Aba01459 Streptoco
	41	11	35.5	20	2	AAQ26927	Aaq26927 Biotinyla
c	42	11	35.5	20	6	ABL45143	Abl45143 Human chr
c	43	11	35.5	20	6	ABK27391	Abk27391 Gamma-ami
c	44	11	35.5	20	12	ADG65356	Adg65356 S1P-4 ant
c	45	11	35.5	20	12	ADG65384	Adg65384 Edg-6 ant

ALIGNMENTS

RESULT 1
ADN36737
ID ADN36737 standard; DNA; 31 BP.
XX
AC ADN36737;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID59.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
DR WPI; 2004-389590/36.
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 18; SEQ ID NO 59; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be

```
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitos, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of an oligonucleotide probe which is related
CC   to the invention.
XX
SQ   Sequence 31 BP; 6 A; 8 C; 11 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 31;  DB 12;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-08;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
              |||||||||||||||||||||||||||||||
Db          1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31


RESULT 2
ADN36746
ID   ADN36746 standard; DNA; 22 BP.
XX
AC   ADN36746;
XX
DT   15-JUL-2004  (first entry)
XX
DE   West Nile virus detection-related PCR primer SeqID68.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; PCR; primer; ss.
XX
OS   West Nile virus.
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
PR   25-NOV-2002; 2002US-0429006P.
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM,  Pollner RB,  Wu W,  Dennis GG,  Darby PM;
XX
DR   WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Claim 26; SEQ ID NO 68; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitos, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of a PCR primer which is related to the
CC   invention.
XX
SQ   Sequence 22 BP; 5 A; 2 C; 10 G; 5 T; 0 U; 0 Other;

  Query Match             71.0%;  Score 22;  DB 12;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.0063;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGAAGTTGAGTAGACGGTGCTG 31
              ||||||||||||||||||||||
Db          1 GGAAGTTGAGTAGACGGTGCTG 22


RESULT 3
ADN36741
ID   ADN36741 standard; DNA; 21 BP.
XX
AC   ADN36741;
XX
DT   15-JUL-2004  (first entry)
XX
DE   West Nile virus detection-related oligonucleotide probe SeqID63.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; probe; ss.
XX
OS   West Nile virus.
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
PR   25-NOV-2002; 2002US-0429006P.
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM,  Pollner RB,  Wu W,  Dennis GG,  Darby PM;
XX
DR   WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Claim 26; SEQ ID NO 63; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitos, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of an oligonucleotide probe which is related
CC   to the invention.
XX
SQ   Sequence 21 BP; 5 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

  Query Match             67.7%;  Score 21;  DB 12;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.024;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGCCACCGGAAGTTGAGTA 21
              |||||||||||||||||||||
Db          1 TCCGCCACCGGAAGTTGAGTA 21
```

```
RESULT 4
ADN36745
ID   ADN36745 standard; DNA; 21 BP.
XX
AC   ADN36745;
XX
DT   15-JUL-2004  (first entry)
XX
DE   West Nile virus detection-related PCR primer SeqID67.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; PCR; primer; ss.
XX
OS   West Nile virus.
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
PR   25-NOV-2002; 2002US-0429006P.
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM,  Pollner RB,  Wu W,  Dennis GG,  Darby PM;
XX
DR   WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Claim 26; SEQ ID NO 67; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitos, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of a PCR primer which is related to the
CC   invention.
XX
SQ   Sequence 21 BP; 5 A; 2 C; 9 G; 5 T; 0 U; 0 Other;

  Query Match             67.7%;  Score 21;  DB 12;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.024;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGAAGTTGAGTAGACGGTGCT 30
              |||||||||||||||||||||
Db          1 GGAAGTTGAGTAGACGGTGCT 21


RESULT 5
ADN36748
ID   ADN36748 standard; DNA; 21 BP.
XX
AC   ADN36748;
XX
DT   15-JUL-2004  (first entry)
XX
DE   West Nile virus detection-related PCR primer SeqID70.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; PCR; primer; ss.
XX
OS   West Nile virus.
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
PR   25-NOV-2002; 2002US-0429006P.
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM,  Pollner RB,  Wu W,  Dennis GG,  Darby PM;
XX
DR   WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Claim 26; SEQ ID NO 70; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitos, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of a PCR primer which is related to the
CC   invention.
XX
SQ   Sequence 21 BP; 5 A; 2 C; 9 G; 5 T; 0 U; 0 Other;

  Query Match             67.7%;  Score 21;  DB 12;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.024;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GAAGTTGAGTAGACGGTGCTG 31
              |||||||||||||||||||||
Db          1 GAAGTTGAGTAGACGGTGCTG 21


RESULT 6
ADN36749
ID   ADN36749 standard; DNA; 20 BP.
XX
AC   ADN36749;
XX
DT   15-JUL-2004  (first entry)
XX
DE   West Nile virus detection-related PCR primer SeqID71.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; PCR; primer; ss.
XX
OS   West Nile virus.
XX
PN   WO2004036190-A2.
XX
```

PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
DR WPI; 2004-389590/36.
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 26; SEQ ID NO 71; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitos, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of a PCR primer which is related to the
CC invention.
XX
SQ Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 64.5%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 AAGTTGAGTAGACGGTGCTG 31
||||||||||||||||||||
Db 1 AAGTTGAGTAGACGGTGCTG 20

RESULT 7
ADN36740
ID ADN36740 standard; DNA; 20 BP.
XX
AC ADN36740;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID62.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
DR WPI; 2004-389590/36.
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 26; SEQ ID NO 62; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitos, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
SQ Sequence 20 BP; 4 A; 6 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 64.5%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAGTTGAGT 20
||||||||||||||||||||
Db 1 TCCGCCACCGGAAGTTGAGT 20

RESULT 8
ADN36747
ID ADN36747 standard; DNA; 20 BP.
XX
AC ADN36747;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related PCR primer SeqID69.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; PCR; primer; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
DR WPI; 2004-389590/36.
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 26; SEQ ID NO 69; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for

CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitos, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of a PCR primer which is related to the
CC invention.
XX
SQ Sequence 20 BP; 5 A; 2 C; 8 G; 5 T; 0 U; 0 Other;

Query Match 64.5%; Score 20; DB 12; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GAAGTTGAGTAGACGGTGCT 30
||||||||||||||||||||
Db 1 GAAGTTGAGTAGACGGTGCT 20

RESULT 9
AEA35007
ID AEA35007 standard; DNA; 20 BP.
XX
AC AEA35007;
XX
DT 28-JUL-2005 (first entry)
XX
DE West Nile virus consensus genome-derived PCR primer, SEQ ID NO:52.
XX
KW Microorganism detection; diagnosis; West Nile virus infection; infection;
KW neurological disease; PCR; primer; ss.
XX
OS West Nile virus; strain NY99-flamingo382-99.
OS West Nile virus; strain NY99-eqhs.
OS West Nile virus; strain HNY1999.
OS West Nile virus; isolate 2741.
OS West Nile virus; isolate WN MD 2000-crow265.
OS West Nile virus; isolate WN NJ 2000 MQ5488.
OS West Nile virus; isolate WN NY 2000-grouse3282.
OS West Nile virus; isolate WN NY 2000-crow3356.
XX
PN WO2005047522-A2.
XX
PD 26-MAY-2005.
XX
PF 10-NOV-2004; 2004WO-US037558.
XX
PR 12-NOV-2003; 2003US-0519096P.
XX
PA (FARB) BAYER HEALTHCARE LLC.
XX
PI Burde SHM, Gierman TM, Glenn CC;
XX
DR WPI; 2005-372389/38.
XX
PT Isolated oligonucleotide for detecting West Nile virus, comprises
PT oligonucleotide sequences.
XX
PS Claim 1; SEQ ID NO 52; 65pp; English.
XX
CC The invention relates to oligonucleotide primers and probes (AEA34957-
CC AEA35014) derived from a West Nile virus consensus sequence (AEA34956).
CC The invention also relates to a method of detecting West Nile virus in a
CC test sample (especially human blood plasma), a test kit comprising one or
CC more oligonucleotides of the invention, and a method for identifying
CC primers for the detection of a nucleic acid sequence. Although West Nile
CC virus rarely kills, about one in 150 people who become infected develop a
CC potentially deadly case of encephalitis or meningitis, and there is
CC currently no means of treatment or prevention of West Nile virus
CC infection. The primers, probes, methods and kits are useful for the
CC effective and early detection of West Nile virus infection, facilitating
CC the diagnosis of infection and the appropriate treatment of symptoms.
CC Sequences AEA34957-AEA35008 represent oligonucleotide primers suitable
CC for use in PCR amplification which are derived from the West Nile virus
CC consensus sequence referred to in the invention (AEA34956).
XX
SQ Sequence 20 BP; 6 A; 4 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 64.5%; Score 20; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCCACCGGAAGTTGAGTAGA 23
||||||||||||||||||||
Db 1 GCCACCGGAAGTTGAGTAGA 20

RESULT 10
ADN36744
ID ADN36744 standard; DNA; 19 BP.
XX
AC ADN36744;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID66.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
DR WPI; 2004-389590/36.
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 26; SEQ ID NO 66; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitos, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
SQ Sequence 19 BP; 5 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

```
  Query Match             61.3%;  Score 19;  DB 12;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.35;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CGCCACCGGAAGTTGAGTA 21
              |||||||||||||||||||
Db          1 CGCCACCGGAAGTTGAGTA 19


RESULT 11
ADN36738
ID   ADN36738 standard; DNA; 19 BP.
XX
AC   ADN36738;
XX
DT   15-JUL-2004  (first entry)
XX
DE   West Nile virus detection-related oligonucleotide probe SeqID60.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; probe; ss.
XX
OS   West Nile virus.
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
PR   25-NOV-2002; 2002US-0429006P.
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM,  Pollner RB,  Wu W,  Dennis GG,  Darby PM;
XX
DR   WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Claim 26; SEQ ID NO 60; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitos, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of an oligonucleotide probe which is related
CC   to the invention.
XX
SQ   Sequence 19 BP; 4 A; 6 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             61.3%;  Score 19;  DB 12;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.35;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGCCACCGGAAGTTGAG 19
              |||||||||||||||||||
Db          1 TCCGCCACCGGAAGTTGAG 19


RESULT 12
ADN36742
ID   ADN36742 standard; DNA; 18 BP.
XX
AC   ADN36742;
XX
DT   15-JUL-2004  (first entry)
XX
DE   West Nile virus detection-related PCR primer SeqID64.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; PCR; primer; ss.
XX
OS   West Nile virus.
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
PR   25-NOV-2002; 2002US-0429006P.
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM,  Pollner RB,  Wu W,  Dennis GG,  Darby PM;
XX
DR   WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Claim 26; SEQ ID NO 64; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitos, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of a PCR primer which is related to the
CC   invention.
XX
SQ   Sequence 18 BP; 4 A; 5 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             58.1%;  Score 18;  DB 12;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CGCCACCGGAAGTTGAGT 20
              ||||||||||||||||||
Db          1 CGCCACCGGAAGTTGAGT 18


RESULT 13
ADN36739
ID   ADN36739 standard; DNA; 19 BP.
XX
AC   ADN36739;
XX
DT   15-JUL-2004  (first entry)
XX
DE   West Nile virus detection-related oligonucleotide probe SeqID61.
XX
KW   hybridisation assay probe; nucleic acid detection;
```

```
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; probe; ss.
XX
OS   West Nile virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= i
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
PR   25-NOV-2002; 2002US-0429006P.
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM,  Pollner RB,  Wu W,  Dennis GG,  Darby PM;
XX
DR   WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Disclosure; SEQ ID NO 61; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitos, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of an oligonucleotide probe which is related
CC   to the invention.
XX
SQ   Sequence 19 BP; 4 A; 6 C; 6 G; 2 T; 0 U; 1 Other;

  Query Match             58.1%;  Score 18;  DB 12;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGCCACCGGAAGTTGAG 19
              ||||||||||||||||||
Db          2 CCGCCACCGGAAGTTGAG 19


RESULT 14
ADN36825/c
ID   ADN36825 standard; RNA; 26 BP.
XX
AC   ADN36825;
XX
DT   15-JUL-2004  (first entry)
XX
DE   West Nile virus detection-related oligonucleotide probe SeqID147.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; probe; ss.
XX
OS   West Nile virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .26
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
PR   25-NOV-2002; 2002US-0429006P.
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM,  Pollner RB,  Wu W,  Dennis GG,  Darby PM;
XX
DR   WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Example 1; SEQ ID NO 147; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitos, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of an oligonucleotide probe which is related
CC   to the invention.
XX
SQ   Sequence 26 BP; 6 A; 10 C; 6 G; 0 T; 4 U; 0 Other;

  Query Match             58.1%;  Score 18;  DB 12;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.3;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 GTTGAGTAGACGGTGCTG 31
              ||||||||||||||||||
Db         26 GTTGAGTAGACGGTGCTG 9


RESULT 15
ADN36743
ID   ADN36743 standard; DNA; 18 BP.
XX
AC   ADN36743;
XX
DT   15-JUL-2004  (first entry)
XX
DE   West Nile virus detection-related oligonucleotide probe SeqID65.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; probe; ss.
XX
OS   West Nile virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
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FT /mod_base= i
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
DR WPI; 2004-389590/36.
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 26; SEQ ID NO 65; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be
CC detected. The hybridisation assay probes and the kits are useful in
CC detecting and amplifying a target nucleic acid sequence, for example
CC flavivirus like West Nile virus, that may be present in a biological
CC sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC birds and culex mosquitos, with humans and horses serving as incidental
CC hosts. Infection of humans can lead to meningitis or encephalitis. The
CC invention may allow for accurate and efficient high throughput screening.
CC The present sequence is that of an oligonucleotide probe which is related
CC to the invention.
XX
SQ Sequence 18 BP; 4 A; 4 C; 6 G; 3 T; 0 U; 1 Other;

Query Match 54.8%; Score 17; DB 12; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCCACCGGAAGTTGAGT 20
||||||||||||||||
Db 2 GCCACCGGAAGTTGAGT 18

Search completed: December 12, 2005, 04:38:26
Job time : 270 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 04:20:28 ; Search time 1949 Seconds
(without alignments)
744.176 Million cell updates/sec

Title: US-10-688-489-59
Perfect score: 31
Sequence: 1 tccgccaccggaagttgagtagacggtgctg 31

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 52288

Minimum DB seq length: 18
Maximum DB seq length: 31

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	12	38.7	27	1	AJ689351	AJ689351 AJ689351
c 2	10	32.3	27	5	BQ540272	BQ540272 PTAM0589
3	10	32.3	27	8	DN955493	DN955493 it88e12.g
c 4	10	32.3	29	10	CZ473162	CZ473162 d03077-3p
c 5	10	32.3	31	3	BM395985	BM395985 5009-0-15
c 6	9	29.0	18	3	BM397227	BM397227 5009-0-3-
c 7	9	29.0	18	3	BM400126	BM400126 5009-0-66
c 8	9	29.0	19	3	BM397047	BM397047 5009-0-28
c 9	9	29.0	19	3	BM397791	BM397791 5009-0-37
c 10	9	29.0	19	3	BM398839	BM398839 5009-0-5-
c 11	9	29.0	19	3	BM398882	BM398882 5009-0-50
c 12	9	29.0	20	1	AJ685250	AJ685250 AJ685250
c 13	9	29.0	20	3	BM397370	BM397370 5009-0-31
c 14	9	29.0	20	3	BM398074	BM398074 5009-0-40
c 15	9	29.0	20	3	BM398469	BM398469 5009-0-45
16	9	29.0	20	10	AJ587566	AJ587566 Arabidops
c 17	9	29.0	21	1	AJ681837	AJ681837 AJ681837
c 18	9	29.0	21	3	BM398235	BM398235 5009-0-42
c 19	9	29.0	21	3	BM400058	BM400058 5009-0-65
c 20	9	29.0	21	3	BM400884	BM400884 5009-0-8-
c 21	9	29.0	21	3	BM401072	BM401072 5009-0-82
c 22	9	29.0	21	9	AZ774560	AZ774560 2M0004H08
c 23	9	29.0	22	1	AJ651078	AJ651078 AJ651078
c 24	9	29.0	22	3	BM395131	BM395131 50072-2-7
c 25	9	29.0	22	3	BM397203	BM397203 5009-0-3-
c 26	9	29.0	22	3	BM398652	BM398652 5009-0-48
c 27	9	29.0	22	3	BM399045	BM399045 5009-0-52
c 28	9	29.0	22	3	BM399148	BM399148 5009-0-54
c 29	9	29.0	22	3	BM400176	BM400176 5009-0-68
c 30	9	29.0	22	3	BM400906	BM400906 5009-0-80
c 31	9	29.0	22	3	BM401082	BM401082 5009-0-82
c 32	9	29.0	22	3	BM401155	BM401155 5009-0-83
c 33	9	29.0	22	8	DR908038	DR908038 CCSEN06F0
34	9	29.0	22	11	TA259H01Q	AL488407 T. brucei
c 35	9	29.0	23	3	BM395136	BM395136 50072-2-7
c 36	9	29.0	23	3	BM395635	BM395635 5009-0-1-
c 37	9	29.0	23	3	BM396314	BM396314 5009-0-2-
c 38	9	29.0	23	3	BM397693	BM397693 5009-0-35
c 39	9	29.0	23	3	BM399213	BM399213 5009-0-55
c 40	9	29.0	23	3	BM399677	BM399677 5009-0-6-
c 41	9	29.0	23	3	BM401179	BM401179 5009-0-83
c 42	9	29.0	23	9	AZ324328	AZ324328 1M0046B16
43	9	29.0	23	9	AZ647047	AZ647047 1M0513B22
44	9	29.0	23	11	TA66H11P	AL458350 T. brucei
c 45	9	29.0	24	3	BM396768	BM396768 5009-0-25

ALIGNMENTS

RESULT 1
AJ689351/c
LOCUS AJ689351 27 bp mRNA linear EST 29-JUN-2004
DEFINITION AJ689351 KN261 Bos taurus cDNA clone KN261-050_N13, mRNA sequence.
ACCESSION AJ689351
VERSION AJ689351.1 GI:49421959
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 27)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI R. Site2: SmaI 3' Seq Primer M13F Normalised library constructed from bovine ovary. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES Location/Qualifiers
source 1. .27
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-050_N13"
/tissue_type="ovary"
/clone_lib="KN261"
/note="Vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2: SmaI; Single pass sequencing. Normalised library constructed from bovine ovary."
ORIGIN

Query Match 38.7%; Score 12; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.3e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          9 CGGAAGTTGAGT 20
              ||||||||||||
Db         16 CGGAAGTTGAGT 5


RESULT 2
BQ540272/c
LOCUS       BQ540272                  27 bp    mRNA    linear   EST 27-MAY-2003
DEFINITION  PTAM0589 Phaeodactylum tricornutum Uni-Zap XR Phaeodactylum
            tricornutum cDNA 5', mRNA sequence.
ACCESSION   BQ540272
VERSION     BQ540272.1  GI:21395842
KEYWORDS    EST.
SOURCE      Phaeodactylum tricornutum
  ORGANISM  Phaeodactylum tricornutum
            Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
            Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Scala,S., Carels,N., Falciatore,A., Chiusano,M.L. and Bowler,C.
  TITLE     Genome properties of the diatom Phaeodactylum tricornutum
  JOURNAL   Plant Physiol. 129 (3), 993-1002 (2002)
   PUBMED   12114555
COMMENT     Contact: Bowler C
            Laboratory of Molecular Plant Biology
            Stazione Zoologica 'Anton Dohrn'
            Villa Comunale, I-80121, Napoli, Italy
            Tel: 39 081 583 3268/3211
            Fax: 39 081 764 1355
            Email: chris@alpha.szn.it
            Seq primer: T3 backward.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Phaeodactylum tricornutum"
                     /mol_type="mRNA"
                     /db_xref="taxon:2850"
                     /cell_line="CCMP632"
                     /clone_lib="Phaeodactylum tricornutum Uni-Zap XR"
                     /note="Vector: Uni-Zap XR vector; Site_1: Eco RI; Site_2:
                     Xho I"
ORIGIN

  Query Match             32.3%;  Score 10;  DB 5;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGCCACCGG 11
              ||||||||||
Db         23 CCGCCACCGG 14


RESULT 3
DN955493
LOCUS       DN955493                  27 bp    mRNA    linear   EST 04-MAY-2005
DEFINITION  it88e12.g1 Gnetum female cone (NYBG) Gnetum gnemon cDNA 3', mRNA
            sequence.
ACCESSION   DN955493
VERSION     DN955493.1  GI:63027631
KEYWORDS    EST.
SOURCE      Gnetum gnemon
  ORGANISM  Gnetum gnemon
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Gnetophyta; Gnetopsida; Gnetales; Gnetaceae; Gnetum.
REFERENCE   1  (bases 1 to 27)
  AUTHORS   Brenner,E.D., Twigg,R.W., Runko,S.J., Katari,M.S., Dedhia,N.N.,
            O'Shaughnessy,A.L., Balija,V., Martienssen,R.A., McCombie,R.W.,
            Benfey,P., Coruzzi,G. and Stevenson,D.
  TITLE     Expressed tag sequences from Gnetum female cone (NYBG)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: W. Richard McCombie
            Lita Annenberg Hazen Genome Sequencing Center
            Cold Spring Harbor Laboratory
            PO Box 100, Cold Spring Harbor, NY 11724, USA
            Tel: 516 367 8884
            Fax: 516 367 8874
            Email: mccombie@cshl.org
            Seq primer: -21M13UnivRev.
FEATURES             Location/Qualifiers
     source          1. .27
                     /organism="Gnetum gnemon"
                     /mol_type="mRNA"
                     /db_xref="taxon:3382"
                     /sex="female"
                     /clone_lib="Gnetum female cone (NYBG)"
                     /note="Organ: mature, unfertilized reproductive strobili;
                     Vector: pBK-CMV; Site_1: XhoI; Site_2: Eco RI; Date:
                     Completed 02/11/02, submitted for sequencing 02/12/02.
                     Library: Stratagene ZAP Express cDNA Synthesis Kit. The
                     library was size-fractionated to enrich for large inserts.
                     Sample: NYBG accession number #436/84"
ORIGIN

  Query Match             32.3%;  Score 10;  DB 8;  Length 27;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCACCGGAA 13
              ||||||||||
Db         12 GCCACCGGAA 21


RESULT 4
CZ473162/c
LOCUS       CZ473162                  29 bp    DNA     linear   GSS 29-APR-2005
DEFINITION  d03077-3prime Exelixis P element XP insertions Drosophila
            melanogaster genomic Sequence recovered from 3' end of P element,
            genomic survey sequence.
ACCESSION   CZ473162
VERSION     CZ473162.1  GI:62967175
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster (fruit fly)
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Thibault,S.T., Singer,M.A., Miyazaki,W.Y., Milash,B., Dompe,N.A.,
            Singh,C.M., Buchholz,R., Demsky,M., Fawcett,R., Francis-Lang,H.L.,
            Ryner,L., Cheung,L.M., Chong,A., Erickson,C., Fisher,W.W.,
            Greer,K., Hartouni,S.R., Howie,E., Jakkula,L., Joo,D., Killpack,K.,
            Laufer,A., Mazzotta,J., Smith,R.D., Stevens,L.M., Stuber,C.,
            Tan,L.R., Ventura,R., Woo,A., Zakrajsek,I., Zhao,L., Chen,F.,
            Swimmer,C., Kopczynski,C., Duyk,G., Winberg,M.L. and Margolis,J.
  TITLE     A complementary transposon tool kit for Drosophila melanogaster
            using P and piggyBac
  JOURNAL   Nat. Genet. 36 (3), 283-287 (2004)
   PUBMED   14981521
COMMENT     Contact: Roger A Hoskins
            Berkeley Drosophila Genome Project
            Lawrence Berkeley National Laboratory
            Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA
            Tel: 510 486 4015
            Fax: 510 486 6798
            Email: RHoskins@lbl.gov
            Sequence recovery method was inverse PCR.
            Sequence orientation is forward strand relative to 5' end of P
            element.
            The P element insertion position is 1 in the 29 bases. This
            insertion position refers to the first base of the 8 base target
            recognition sequence.
            Class: transposon insertion site.
FEATURES             Location/Qualifiers
     source          1. .29
                     /organism="Drosophila melanogaster"
                     /mol_type="genomic DNA"
                     /strain="isogenic w- strain"
                     /db_xref="taxon:7227"
```

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                     /clone_lib="Exelixis P element XP insertions"
                     /note="Vector: P element XP (GenBank accession number
                     AY515149); An isogenic w- Drosophila melanogaster strain
                     was mutagenized by remobilization of transposable
                     elements. For the P element XP, we selected an easily
                     mobilized ammunition element among inserts hopped onto the
                     Binsinscy balancer. New insertions were collected in vials
                     from dysgenic females using the standard chromosomal
                     source of transposase, delta2-3. All lines were mapped to
                     a chromosome by standard genetic methods, examined for
                     homozygous viability and used for recovery of flanking
                     genomic sequence by inverse PCR."
ORIGIN

  Query Match             32.3%;  Score 10;  DB 10;  Length 29;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GTAGACGGTG 28
              ||||||||||
Db         14 GTAGACGGTG 5


RESULT 5
BM395985/c
LOCUS       BM395985                  31 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-15-C03.t.2 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM395985
VERSION     BM395985.1  GI:18196038
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 31)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .31
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

  Query Match             32.3%;  Score 10;  DB 3;  Length 31;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGCCACCG 10
              ||||||||||
Db         24 TCCGCCACCG 15


RESULT 6
BM397227/c
LOCUS       BM397227                  18 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-3-F09.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM397227
VERSION     BM397227.1  GI:18197280
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: BlueScript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

  Query Match             29.0%;  Score 9;  DB 3;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.5e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGCCACCG 10
              |||||||||
Db         17 CCGCCACCG 9


RESULT 7
BM400126/c
LOCUS       BM400126                  18 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-66-G02.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM400126
VERSION     BM400126.1  GI:18200179
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
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/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

Query Match 29.0%; Score 9; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCCACCG 10
||||||||||
Db 18 CCGCCACCG 10

RESULT 8
BM397047/c
LOCUS BM397047 19 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-28-D04.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397047
VERSION BM397047.1 GI:18197100
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE 1 (bases 1 to 19)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES Location/Qualifiers
source 1. .19
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

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Db 19 CCGCCACCG 11

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Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM397791
VERSION BM397791.1 GI:18197844
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE 1 (bases 1 to 19)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
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preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

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Qy 2 CCGCCACCG 10
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Db 18 CCGCCACCG 10

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LOCUS BM398839 19 bp mRNA linear EST 17-JAN-2002
DEFINITION 5009-0-5-F03.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM398839
VERSION BM398839.1 GI:18198892
KEYWORDS EST.
SOURCE Tetrahymena thermophila
ORGANISM Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE 1 (bases 1 to 19)
AUTHORS Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL Unpublished (2002)
COMMENT Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
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/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

Query Match 29.0%; Score 9; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;

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Db         11 CCGCCACCG 3


RESULT 11
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LOCUS       BM398882                 19 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-50-A08.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM398882
VERSION     BM398882.1  GI:18198935
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
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                     /organism="Tetrahymena thermophila"
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                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

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Qy          2 CCGCCACCG 10
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Db         18 CCGCCACCG 10


RESULT 12
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DEFINITION  AJ685250 CSEQRAN04 Sus scrofa cDNA clone C0001808_F16, mRNA
            sequence.
ACCESSION   AJ685250
VERSION     AJ685250.1  GI:49417840
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
            Sus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
            R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
            from pig uterus. Clones available from UK Centre for Functional
            Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
            EH25 9PS, www.arkgenomics.org.
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          2 CCGCCACCG 10
              |||||||||
Db         11 CCGCCACCG 3


RESULT 13
BM397370/c
LOCUS       BM397370                 20 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-31-H04.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM397370
VERSION     BM397370.1  GI:18197423
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
FEATURES             Location/Qualifiers
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                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

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Qy          2 CCGCCACCG 10
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Db         19 CCGCCACCG 11


RESULT 14
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LOCUS       BM398074                 20 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-40-B03.t.1 Chilcoat/Turkewitz cDNA (large fraction)
            Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION   BM398074
VERSION     BM398074.1  GI:18198127
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
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                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

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RESULT 15
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LOCUS       BM398469                 20 bp    mRNA    linear   EST 17-JAN-2002
DEFINITION  5009-0-45-F11.t.2 Chilcoat/Turkewitz cDNA (large fraction)
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ACCESSION   BM398469
VERSION     BM398469.1  GI:18198522
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
  ORGANISM  Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymenidae; Tetrahymena.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
  TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
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                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN

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Qy          2 CCGCCACCG 10
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Job time : 1951 secs
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 04:27:38 ; Search time 93 Seconds
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Title: US-10-688-489-59
Perfect score: 31
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

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Minimum DB seq length: 18
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	3	12	38.7	25	3	US-09-396-196G-116541	Sequence 116541,
c	4	11	35.5	19	6	PCT-US93-09232-14	Sequence 14, Appl
c	5	11	35.5	22	3	US-09-811-838-20	Sequence 20, Appl
c	6	11	35.5	24	2	US-08-229-781-14	Sequence 14, Appl
c	7	11	35.5	24	2	US-08-630-918-14	Sequence 14, Appl
c	8	11	35.5	24	3	US-09-004-422-14	Sequence 14, Appl
c	9	11	35.5	24	3	US-09-918-568-14	Sequence 14, Appl
c	10	11	35.5	24	3	US-10-126-120-3	Sequence 3, Appli
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c	44	10	32.3	20	2	US-08-313-185-22	Sequence 22, Appl
c	45	10	32.3	20	2	US-08-649-046-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-396-196G-116529/c
; Sequence 116529, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 116529
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-116529

Query Match 38.7%; Score 12; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
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; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17

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;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 116530
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-116530

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; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
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;  SOFTWARE: FastSEQ for Windows Version 4.0
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;   TYPE: DNA
;   ORGANISM: mus musculus
US-09-396-196G-116541

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RESULT 4
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; Sequence 14, Application PC/TUS9309232
;  GENERAL INFORMATION:
;    APPLICANT:  The Upjohn
;    APPLICANT:  Company
;    TITLE OF INVENTION:  Somatotropin Modifications
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Corporate Intellectual Property Law
;      STREET:  301 Henrietta Street
;      CITY:  Kalamazoo
;      STATE:  Michigan
;      COUNTRY:  USA
;      ZIP:  49001
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" diskette (DS, HD 2.0 Mb)
;      COMPUTER:  IBM PC compatible WIN 386
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/09232
;      FILING DATE:  ,        ,
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  James D. Darnley, Jr.
;      REGISTRATION NUMBER:  33673
;      REFERENCE/DOCKET NUMBER:  4766.P CN1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  616  385  5210
;      TELEFAX:  616  385  6897
;      TELEX:  224  401  UPJOHN
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleotide
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US93-09232-14

  Query Match             35.5%;  Score 11;  DB 6;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 5.6e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GTAGACGGTGC 29
              ||||||||||||
Db         16 GTAGACGGTGC 6


RESULT 5
US-09-811-838-20/c
; Sequence 20, Application US/09811838
; Patent No. 6875757
; GENERAL INFORMATION:
;  APPLICANT: Miller, Duane D.
;  APPLICANT:  Tigyi, Gabor
;  APPLICANT:  Dalton, James T.
;  APPLICANT:  Sardar, Vineet M.
;  APPLICANT:  Elrod, Don B.
;  APPLICANT:  Xu, Huiping
;  APPLICANT:  Baker, Daniel L.
;  APPLICANT:  Wang, Dean
;  APPLICANT:  Liliom, Karoly
;  APPLICANT:  Fischer, David J.
;  APPLICANT:  Virag, Tamas
;  APPLICANT:  Nusser, No. 6875757a
;  TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
;  TITLE OF INVENTION:  USE
;  FILE REFERENCE: 20609/181
;  CURRENT APPLICATION NUMBER: US/09/811,838
;  CURRENT FILING DATE:  2001-03-19
;  PRIOR APPLICATION NUMBER: 60/190,370
;  PRIOR FILING DATE: 2000-03-17
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  primer,
;   OTHER INFORMATION: reverse EDG-6
US-09-811-838-20

  Query Match             35.5%;  Score 11;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 AGACGGTGCTG 31
              ||||||||||||
Db         17 AGACGGTGCTG 7


RESULT 6
```

```
US-08-229-781-14/c
; Sequence 14, Application US/08229781
; Patent No. 5589174
;  GENERAL INFORMATION:
;    APPLICANT:  Yoshinobu OKUNO et al.
;    TITLE OF INVENTION:  ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/229,781
;      FILING DATE:  April 19, 1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/054,016
;      FILING DATE:  April 29, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid (synthetic DNA)
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:
;      CELL LINE:
;      ORGANELLE:
;    IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:
;      MAP POSITION:
;      UNITS:
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      DOCUMENT NUMBER:
;      FILING DATE:
;      PUBLICATION DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:
US-08-229-781-14

  Query Match             35.5%;  Score 11;  DB 2;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AGTTGAGTAGA 23
              ||||||||||
Db         12 AGTTGAGTAGA 2


RESULT 7
US-08-630-918-14/c
; Sequence 14, Application US/08630918
; Patent No. 5631350
;  GENERAL INFORMATION:
;    APPLICANT:  Yoshinobu OKUNO et al.
;    TITLE OF INVENTION:  ANTI-HUMAN INFLUENZA VIRUS ANTIBODY
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack
;      STREET:  805 Fifteenth Street, N.W., #700
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/630,918
;      FILING DATE:  April 5, 1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/229,781
;      FILING DATE:  April 19, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/054,016
;      FILING DATE:  April 29, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-8850
;      TELEFAX:
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid (synthetic DNA)
US-08-630-918-14

  Query Match             35.5%;  Score 11;  DB 2;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AGTTGAGTAGA 23
              ||||||||||
Db         12 AGTTGAGTAGA 2


RESULT 8
```

```
US-09-004-422-14/c
; Sequence 14, Application US/09004422
; Patent No. 6337070
;  GENERAL INFORMATION:
;    APPLICANT:  Yoshinobu OKUNO et al.
;    TITLE OF INVENTION:  POLYPEPTIDES FOR USE IN GENERATING
;    TITLE OF INVENTION:  ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wenderoth, Lind & Ponack, L.L.P.
;      STREET:  2033 K Street, N.W., #800
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20006
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 mb
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  Wordperfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/004,422
;      FILING DATE:  January 8, 1998
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/443,862
;      FILING DATE:  May 22, 1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/229,781
;      FILING DATE:  April 19, 1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/054,016
;      FILING DATE:  April 29, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warren M. Cheek, Jr.
;      REGISTRATION NUMBER:  33,367
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-721-8200
;      TELEFAX:  202-721-8250
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 bases
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid (synthetic DNA)
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:
;      STRAIN:
;      INDIVIDUAL ISOLATE:
;      DEVELOPMENTAL STAGE:
;      HAPLOTYPE:
;      TISSUE TYPE:
;      CELL TYPE:
;      CELL LINE:
;      ORGANELLE:
;    IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:
;    POSITION IN GENOME:
;      CHROMOSOME/SEGMENT:
;      MAP POSITION:
;      UNITS:
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
;      IDENTIFICATION METHOD:
;      OTHER INFORMATION:
;    PUBLICATION INFORMATION:
;      AUTHORS:
;      TITLE:
;      JOURNAL:
;      VOLUME:
;      ISSUE:
;      PAGES:
;      DATE:
;      DOCUMENT NUMBER:
;      FILING DATE:
;      PUBLICATION DATE:
;      RELEVANT RESIDUES IN SEQ ID NO:
US-09-004-422-14

  Query Match             35.5%;  Score 11;  DB 3;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AGTTGAGTAGA 23
               ||||||||||| 
Db         12 AGTTGAGTAGA 2


RESULT 9
US-09-918-568-14/c
; Sequence 14, Application US/09918568
; Patent No. 6720409
;  GENERAL INFORMATION:
;       APPLICANT: Yoshinobu OKUNO et al.
;       TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING
;                           ANTI-HUMAN INFLUENZA VIRUS ANTIBODIES (AS AMENDED)
;       NUMBER OF SEQUENCES: 58
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
;            STREET: 2033 K Street, N.W., #800
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: U.S.A.
;            ZIP: 20006
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: MS-DOS
;            SOFTWARE: Wordperfect 5.1
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/918,568
;            FILING DATE: 02-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/004,422
;            FILING DATE: January 8, 1998
;            APPLICATION NUMBER: 08/443,862
;            FILING DATE: May 22, 1995
;            APPLICATION NUMBER: 08/229,781
;            FILING DATE: April 19, 1994
;            APPLICATION NUMBER: 08/054,016
;            FILING DATE: April 29, 1993
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Warren M. Cheek, Jr.
;            REGISTRATION NUMBER: 33,367
;            REFERENCE/DOCKET NUMBER: <Unknown>
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-721-8200
;            TELEFAX: 202-721-8250
;            TELEX: <Unknown>
;  INFORMATION FOR SEQ ID NO: 14:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 24 bases
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid (synthetic DNA)
;       HYPOTHETICAL: <Unknown>
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;       ANTI-SENSE: <Unknown>
;       FRAGMENT TYPE: <Unknown>
;       ORIGINAL SOURCE:
;            ORGANISM: <Unknown>
;            STRAIN: <Unknown>
;            INDIVIDUAL ISOLATE: <Unknown>
;            DEVELOPMENTAL STAGE: <Unknown>
;            HAPLOTYPE: <Unknown>
;            TISSUE TYPE: <Unknown>
;            CELL TYPE: <Unknown>
;            CELL LINE: <Unknown>
;            ORGANELLE: <Unknown>
;       IMMEDIATE SOURCE:
;            LIBRARY: <Unknown>
;            CLONE: <Unknown>
;       POSITION IN GENOME:
;            CHROMOSOME/SEGMENT: <Unknown>
;            MAP POSITION: <Unknown>
;            UNITS: <Unknown>
;       FEATURE:
;            NAME/KEY:
;            LOCATION:
;            IDENTIFICATION METHOD:
;            OTHER INFORMATION:
;       PUBLICATION INFORMATION:
;            AUTHORS:
;            TITLE:
;            JOURNAL:
;            VOLUME:
;            ISSUE:
;            PAGES:
;            DATE:
;            DOCUMENT NUMBER:
;            FILING DATE:
;            PUBLICATION DATE:
;            RELEVANT RESIDUES IN SEQ ID NO:
;       SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-918-568-14

  Query Match            35.5%;  Score 11;  DB 3;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 5.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 AGTTGAGTAGA 23
              ||||||||||
Db         12 AGTTGAGTAGA 2


RESULT 10
US-10-126-120-3/c
; Sequence 3, Application US/10126120
; Patent No. 6893825
; GENERAL INFORMATION:
;  APPLICANT: Sakakibara, Hitoshi
;  APPLICANT:  Takei, Kentaro
;  TITLE OF INVENTION: MICROORGANISMS FOR USE IN THE MEASUREMENT OF ENVIRONMENTAL FACTOR
;  FILE REFERENCE: 11127-004001
;  CURRENT APPLICATION NUMBER: US/10/126,120
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: JP 2001-291059
;  PRIOR FILING DATE: 2001-09-25
;  NUMBER OF SEQ ID NOS: 50
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC DNA
US-10-126-120-3

  Query Match            35.5%;  Score 11;  DB 3;  Length 24;
  Best Local Similarity  100.0%;  Pred. No. 5.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGAAGTTGAGT 20
              ||||||||||
Db         21 GGAAGTTGAGT 11


RESULT 11
US-08-118-200-5
; Sequence 5, Application US/08118200
; Patent No. 6197500
;  GENERAL INFORMATION:
;    APPLICANT:  SUTHERLAND, Grant R
;    APPLICANT:  RICHARDS, Robert I
;    APPLICANT:  SCHLESSINGER, David
;    APPLICANT:  NAGARAJA, Ramaiah
;    APPLICANT:  KREMER, Eric J
;    APPLICANT:  YU, Sui
;    APPLICANT:  BAKER, Elizabeth
;    APPLICANT:  MULLEY, John C
;    APPLICANT:  MANDEL, Jean-Louis
;    APPLICANT:  PRITCHARD, Melanie April
;    APPLICANT:  LYNCH, Michael
;    TITLE OF INVENTION:  DNA SEQUENCES RELATED TO ISOLATED
;    TITLE OF INVENTION:  FRAGILE X SYNDROME
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/118,200
;      FILING DATE:  09-SEP-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/802,650
;      FILING DATE:  05-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/672,232
;      FILING DATE:  20-MAR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/638,518
;      FILING DATE:  04-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/966,517
;      FILING DATE:  23-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Crane-Feury, Sharon E
;      REGISTRATION NUMBER:  36,113
;      REFERENCE/DOCKET NUMBER:  020160-164
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-118-200-5

  Query Match            35.5%;  Score 11;  DB 3;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 5.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          8 CCGGAAGTTGA 18
              ||||||||||
Db          8 CCGGAAGTTGA 18


RESULT 12
US-08-458-745-5
; Sequence 5, Application US/08458745
; Patent No. 6242576
;  GENERAL INFORMATION:
;    APPLICANT:  SUTHERLAND, Grant R
;    APPLICANT:  RICHARDS, Robert I
;    APPLICANT:  SCHLESSINGER, David
;    APPLICANT:  NAGARAJA, Ramaiah
;    APPLICANT:  KREMER, Eric J
;    APPLICANT:  YU, Sui
;    APPLICANT:  BAKER, Elizabeth
;    APPLICANT:  MULLEY, John C
;    APPLICANT:  MANDEL, Jean-Louis
;    APPLICANT:  PRITCHARD, Melanie April
;    APPLICANT:  LYNCH, Michael
;    TITLE OF INVENTION:  DNA SEQUENCES RELATED TO ISOLATED
;    TITLE OF INVENTION:  FRAGILE X SYNDROME
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;      STREET:  P.O. Box 1404
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  United States
;      ZIP:  22313-1404
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,745
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/118,200
;      FILING DATE:  09-SEP-1993
;      APPLICATION NUMBER:  US 07/802,650
;      FILING DATE:  05-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/672,232
;      FILING DATE:  20-MAR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/638,518
;      FILING DATE:  04-JAN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/966,517
;      FILING DATE:  23-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Crane-Feury, Sharon E
;      REGISTRATION NUMBER:  36,113
;      REFERENCE/DOCKET NUMBER:  020160-164
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 836-6620
;      TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-458-745-5

  Query Match           35.5%;  Score 11;  DB 3;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 5.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CCGGAAGTTGA 18
              ||||||||||
Db          8 CCGGAAGTTGA 18


RESULT 13
US-09-876-176-5/c
; Sequence 5, Application US/09876176
; Patent No. 6586244
; GENERAL INFORMATION:
;  APPLICANT: Reinhard, Christoph
;  APPLICANT:  Jefferson, Anne B.
;  APPLICANT:  Den-Otter, Douglas R.
;  APPLICANT:  Winter, Jill A.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
;  TITLE OF INVENTION:  NEOPLASTIC DISEASE USING INHIBITORS OF LAMININ5BETA3
;  FILE REFERENCE: PP-01702.002/200130.523
;  CURRENT APPLICATION NUMBER: US/09/876,176
;  CURRENT FILING DATE:  2001-06-06
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Control oligonucleotide
US-09-876-176-5

  Query Match           35.5%;  Score 11;  DB 3;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 5.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGAAGTTGAGT 20
              ||||||||||
Db         20 GGAAGTTGAGT 10


RESULT 14
US-09-396-196G-20729
; Sequence 20729, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20729
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-396-196G-20729

  Query Match           35.5%;  Score 11;  DB 3;  Length 25;
  Best Local Similarity  100.0%;  Pred. No. 5.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 AGACGGTGCTG 31
              ||||||||||
Db         10 AGACGGTGCTG 20


RESULT 15
```

```
US-09-396-196G-20730
; Sequence 20730, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
;  APPLICANT: Michael Mittmann
;  APPLICANT:  David Mack
;  APPLICANT:  David Lockhart
;  APPLICANT:  Affymetrix, Inc.
;  TITLE OF INVENTION: Methods of Genetic Analysis
;  FILE REFERENCE: 3101.1
;  CURRENT APPLICATION NUMBER: US/09/396,196G
;  CURRENT FILING DATE:  1999-09-15
;  PRIOR APPLICATION NUMBER: 60/100,678
;  PRIOR FILING DATE: 1998-09-17
;  NUMBER OF SEQ ID NOS: 127806
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20730
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-396-196G-20730

  Query Match             35.5%;  Score 11;  DB 3;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 5.5e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         21 AGACGGTGCTG 31
              ||||||||||| 
Db          6 AGACGGTGCTG 16


Search completed: December 12, 2005, 05:41:02
Job time : 93 secs
```

OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 05:06:54 ; Search time 419 Seconds
(without alignments)
611.816 Million cell updates/sec

Title: US-10-688-489-59
Perfect score: 31
Sequence: 1 tccgccaccggaagttgagtagacggtgctg 31

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9450414

Minimum DB seq length: 18
Maximum DB seq length: 31

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	31	100.0	31	8	US-10-688-489-59	Sequence 59, Appl
	2	22	71.0	22	8	US-10-688-489-68	Sequence 68, Appl
	3	21	67.7	21	8	US-10-688-489-63	Sequence 63, Appl
	4	21	67.7	21	8	US-10-688-489-67	Sequence 67, Appl
	5	21	67.7	21	8	US-10-688-489-70	Sequence 70, Appl
	6	20	64.5	20	8	US-10-688-489-62	Sequence 62, Appl
	7	20	64.5	20	8	US-10-688-489-69	Sequence 69, Appl
	8	20	64.5	20	8	US-10-688-489-71	Sequence 71, Appl
	9	20	64.5	20	9	US-10-985-805-52	Sequence 52, Appl
	10	19	61.3	19	8	US-10-688-489-60	Sequence 60, Appl
	11	19	61.3	19	8	US-10-688-489-66	Sequence 66, Appl
	12	18	58.1	18	8	US-10-688-489-64	Sequence 64, Appl
	13	18	58.1	19	8	US-10-688-489-61	Sequence 61, Appl
c	14	18	58.1	26	8	US-10-688-489-147	Sequence 147, App
	15	17	54.8	18	8	US-10-688-489-65	Sequence 65, Appl
	16	15	48.4	21	8	US-10-688-489-104	Sequence 104, App
	17	15	48.4	22	8	US-10-688-489-185	Sequence 185, App
	18	15	48.4	25	5	US-10-098-263B-27587	Sequence 27587, A
	19	15	48.4	28	8	US-10-688-489-186	Sequence 186, App
c	20	14	45.2	25	10	US-11-036-317-721195	Sequence 721195,
c	21	13	41.9	18	6	US-10-265-689-39	Sequence 39, Appl
	22	13	41.9	19	8	US-10-688-489-105	Sequence 105, App
	23	13	41.9	21	9	US-10-871-841-48	Sequence 48, Appl
c	24	13	41.9	25	7	US-10-719-956-465218	Sequence 465218,
c	25	13	41.9	25	8	US-10-719-900-67606	Sequence 67606, A
c	26	13	41.9	25	8	US-10-719-900-228204	Sequence 228204,
c	27	13	41.9	25	8	US-10-719-900-380938	Sequence 380938,
c	28	13	41.9	25	10	US-11-036-317-845552	Sequence 845552,
	29	12	38.7	18	8	US-10-688-489-178	Sequence 178, App
	30	12	38.7	18	8	US-10-688-489-181	Sequence 181, App
	31	12	38.7	21	10	US-11-110-517-1	Sequence 1, Appli
	32	12	38.7	25	5	US-10-098-263B-48220	Sequence 48220, A
	33	12	38.7	25	5	US-10-098-263B-55468	Sequence 55468, A
c	34	12	38.7	25	5	US-10-098-263B-84603	Sequence 84603, A
c	35	12	38.7	25	5	US-10-098-263B-84604	Sequence 84604, A
c	36	12	38.7	25	5	US-10-098-263B-101297	Sequence 101297,
	37	12	38.7	25	5	US-10-098-263B-130532	Sequence 130532,
c	38	12	38.7	25	7	US-10-719-956-87744	Sequence 87744, A
c	39	12	38.7	25	7	US-10-719-956-109527	Sequence 109527,
c	40	12	38.7	25	7	US-10-719-956-243826	Sequence 243826,
c	41	12	38.7	25	7	US-10-719-956-447257	Sequence 447257,
c	42	12	38.7	25	7	US-10-719-956-599493	Sequence 599493,
c	43	12	38.7	25	7	US-10-719-956-623888	Sequence 623888,
	44	12	38.7	25	7	US-10-719-956-672084	Sequence 672084,
c	45	12	38.7	25	8	US-10-719-900-21898	Sequence 21898, A

ALIGNMENTS

RESULT 1
US-10-688-489-59
; Sequence 59, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 31
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-59

Query Match 100.0%; Score 31; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31
||||||||||||||||||||||||||||||
Db 1 TCCGCCACCGGAAGTTGAGTAGACGGTGCTG 31

RESULT 2
US-10-688-489-68
; Sequence 68, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen

```
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 68
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-68

  Query Match             71.0%;  Score 22;  DB 8;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.0046;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGAAGTTGAGTAGACGGTGCTG 31
               ||||||||||||||||||||||
Db          1 GGAAGTTGAGTAGACGGTGCTG 22


RESULT 3
US-10-688-489-63
; Sequence 63, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 63
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-63

  Query Match             67.7%;  Score 21;  DB 8;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.018;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGCCACCGGAAGTTGAGTA 21
              |||||||||||||||||||||
Db          1 TCCGCCACCGGAAGTTGAGTA 21


RESULT 4
US-10-688-489-67
; Sequence 67, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 67
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-67

  Query Match             67.7%;  Score 21;  DB 8;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.018;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGAAGTTGAGTAGACGGTGCT 30
               |||||||||||||||||||||
Db          1 GGAAGTTGAGTAGACGGTGCT 21


RESULT 5
US-10-688-489-70
; Sequence 70, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 70
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-70

  Query Match             67.7%;  Score 21;  DB 8;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.018;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 GAAGTTGAGTAGACGGTGCTG 31
               |||||||||||||||||||||
Db          1 GAAGTTGAGTAGACGGTGCTG 21


RESULT 6
US-10-688-489-62
```

; Sequence 62, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-62

Query Match 64.5%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCCACCGGAAGTTGAGT 20
||||||||||||||||||||
Db 1 TCCGCCACCGGAAGTTGAGT 20

RESULT 7
US-10-688-489-69
; Sequence 69, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 69
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-69

Query Match 64.5%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GAAGTTGAGTAGACGGTGCT 30
||||||||||||||||||||
Db 1 GAAGTTGAGTAGACGGTGCT 20

RESULT 8
US-10-688-489-71
; Sequence 71, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 71
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-71

Query Match 64.5%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 AAGTTGAGTAGACGGTGCTG 31
||||||||||||||||||||
Db 1 AAGTTGAGTAGACGGTGCTG 20

RESULT 9
US-10-985-805-52
; Sequence 52, Application US/10985805
; Publication No. US20050130133A1
; GENERAL INFORMATION:
; APPLICANT: Burde, Stefan H.M.
; APPLICANT: Gierman, Todd M.
; APPLICANT: Glenn, Christopher C.
; TITLE OF INVENTION: Oligonucleotides and Methods for Detection of West Nile Virus
; FILE REFERENCE: 7430*201
; CURRENT APPLICATION NUMBER: US/10/985,805
; CURRENT FILING DATE: 2004-11-10
; PRIOR APPLICATION NUMBER: US 60/519,096
; PRIOR FILING DATE: 2003-11-12
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 20
; TYPE: DNA
; ORGANISM: West Nile virus
US-10-985-805-52

Query Match 64.5%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCCACCGGAAGTTGAGTAGA 23
||||||||||||||||||||
Db 1 GCCACCGGAAGTTGAGTAGA 20

RESULT 10
US-10-688-489-60
; Sequence 60, Application US/10688489

```
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 60
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-60

  Query Match             61.3%;  Score 19;  DB 8;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGCCACCGGAAGTTGAG 19
              |||||||||||||||||||
Db          1 TCCGCCACCGGAAGTTGAG 19


RESULT 11
US-10-688-489-66
; Sequence 66, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 66
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-66

  Query Match             61.3%;  Score 19;  DB 8;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.28;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CGCCACCGGAAGTTGAGTA 21
              |||||||||||||||||||
Db          1 CGCCACCGGAAGTTGAGTA 19


RESULT 12
US-10-688-489-64
; Sequence 64, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 64
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-64

  Query Match             58.1%;  Score 18;  DB 8;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CGCCACCGGAAGTTGAGT 20
              ||||||||||||||||||
Db          1 CGCCACCGGAAGTTGAGT 18


RESULT 13
US-10-688-489-61
; Sequence 61, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 61
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: West Nile Virus
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: I
US-10-688-489-61

  Query Match             58.1%;  Score 18;  DB 8;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
```

```
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGCCACCGGAAGTTGAG 19
              ||||||||||||||||||
Db          2 CCGCCACCGGAAGTTGAG 19


RESULT 14
US-10-688-489-147/c
; Sequence 147, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 147
;   LENGTH: 26
;   TYPE: RNA
;   ORGANISM: West Nile Virus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(26)
;   OTHER INFORMATION: 2'-OMe nucleotide analogs
US-10-688-489-147

  Query Match             58.1%;  Score 18;  DB 8;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 1.1;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 GTTGAGTAGACGGTGCTG 31
              ||||||||||||||||||
Db         26 GTTGAGTAGACGGTGCTG 9


RESULT 15
US-10-688-489-65
; Sequence 65, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 65
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: West Nile Virus
;   FEATURE:
;   NAME/KEY: modified_base
;   LOCATION: (1)...(1)
;   OTHER INFORMATION: I
US-10-688-489-65

  Query Match             54.8%;  Score 17;  DB 8;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 4.4;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GCCACCGGAAGTTGAGT 20
              |||||||||||||||||
Db          2 GCCACCGGAAGTTGAGT 18


Search completed: December 12, 2005, 06:38:57
Job time : 419 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 05:39:28 ; Search time 119 Seconds
(without alignments)
97.391 Million cell updates/sec

Title: US-10-688-489-59
Perfect score: 31
Sequence: 1 tccgccaccggaagttgagtagacggtgctg 31

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3392430 seqs, 186927314 residues

Word size : 0

Total number of hits satisfying chosen parameters: 6558440

Minimum DB seq length: 18
Maximum DB seq length: 31

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13	41.9	19	8	US-11-101-244-893396	Sequence 893396,
c	2	13	41.9	19	8	US-11-101-244-1142294	Sequence 1142294,
c	3	13	41.9	19	8	US-11-101-244-1558548	Sequence 1558548,
	4	13	41.9	19	9	US-11-083-784-893396	Sequence 893396,
c	5	13	41.9	19	9	US-11-083-784-1142294	Sequence 1142294,
c	6	13	41.9	19	9	US-11-083-784-1558548	Sequence 1558548,
c	7	12	38.7	19	8	US-11-101-244-203873	Sequence 203873,
c	8	12	38.7	19	8	US-11-101-244-203933	Sequence 203933,
c	9	12	38.7	19	8	US-11-101-244-252961	Sequence 252961,
	10	12	38.7	19	8	US-11-101-244-289277	Sequence 289277,
	11	12	38.7	19	8	US-11-101-244-301698	Sequence 301698,
	12	12	38.7	19	8	US-11-101-244-730807	Sequence 730807,
	13	12	38.7	19	8	US-11-101-244-734540	Sequence 734540,
c	14	12	38.7	19	8	US-11-101-244-769352	Sequence 769352,
c	15	12	38.7	19	8	US-11-101-244-769426	Sequence 769426,
c	16	12	38.7	19	8	US-11-101-244-941002	Sequence 941002,
c	17	12	38.7	19	8	US-11-101-244-941012	Sequence 941012,
	18	12	38.7	19	8	US-11-101-244-1104174	Sequence 1104174,
	19	12	38.7	19	8	US-11-101-244-1104183	Sequence 1104183,
	20	12	38.7	19	8	US-11-101-244-1339290	Sequence 1339290,
c	21	12	38.7	19	8	US-11-101-244-1360771	Sequence 1360771,
	22	12	38.7	19	8	US-11-101-244-1370517	Sequence 1370517,
c	23	12	38.7	19	8	US-11-101-244-1513933	Sequence 1513933,
c	24	12	38.7	19	8	US-11-101-244-1550584	Sequence 1550584,
c	25	12	38.7	19	8	US-11-101-244-1550586	Sequence 1550586,
c	26	12	38.7	19	8	US-11-101-244-1550608	Sequence 1550608,
c	27	12	38.7	19	9	US-11-083-784-203873	Sequence 203873,
c	28	12	38.7	19	9	US-11-083-784-203933	Sequence 203933,
c	29	12	38.7	19	9	US-11-083-784-252961	Sequence 252961,
	30	12	38.7	19	9	US-11-083-784-289277	Sequence 289277,
	31	12	38.7	19	9	US-11-083-784-301698	Sequence 301698,
	32	12	38.7	19	9	US-11-083-784-730807	Sequence 730807,
	33	12	38.7	19	9	US-11-083-784-734540	Sequence 734540,
c	34	12	38.7	19	9	US-11-083-784-769352	Sequence 769352,
c	35	12	38.7	19	9	US-11-083-784-769426	Sequence 769426,
c	36	12	38.7	19	9	US-11-083-784-941002	Sequence 941002,
c	37	12	38.7	19	9	US-11-083-784-941012	Sequence 941012,
	38	12	38.7	19	9	US-11-083-784-1104174	Sequence 1104174,
	39	12	38.7	19	9	US-11-083-784-1104183	Sequence 1104183,
	40	12	38.7	19	9	US-11-083-784-1339290	Sequence 1339290,
c	41	12	38.7	19	9	US-11-083-784-1360771	Sequence 1360771,
	42	12	38.7	19	9	US-11-083-784-1370517	Sequence 1370517,
c	43	12	38.7	19	9	US-11-083-784-1513933	Sequence 1513933,
c	44	12	38.7	19	9	US-11-083-784-1550584	Sequence 1550584,
c	45	12	38.7	19	9	US-11-083-784-1550586	Sequence 1550586,

ALIGNMENTS

RESULT 1
US-11-101-244-893396
; Sequence 893396, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 893396
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-893396

Query Match 41.9%; Score 13; DB 8; Length 19;
Best Local Similarity 84.6%; Pred. No. 98;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
Qy          7 ACCGGAAGTTGAG 19
              ||||||||::|||
Db          2 ACCGGAAGUUGAG 14
```

RESULT 2
US-11-101-244-1142294/c
; Sequence 1142294, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

```
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1142294
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1142294

  Query Match             41.9%;  Score 13;  DB 8;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GTAGACGGTGCTG 31
              |||||||||||||
Db         16 GTAGACGGTGCTG 4


RESULT 3
US-11-101-244-1558548/c
; Sequence 1558548, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1558548
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-1558548

  Query Match             41.9%;  Score 13;  DB 8;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGAAGTTGAGTAG 22
              |||||||||||||
Db         13 GGAAGTTGAGTAG 1


RESULT 4
US-11-083-784-893396
; Sequence 893396, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 893396
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-893396

  Query Match             41.9%;  Score 13;  DB 9;  Length 19;
  Best Local Similarity   84.6%;  Pred. No. 98;
  Matches   11;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 ACCGGAAGTTGAG 19
              ||||||||::|||
Db          2 ACCGGAAGUUGAG 14


RESULT 5
US-11-083-784-1142294/c
; Sequence 1142294, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 1142294
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-1142294

  Query Match             41.9%;  Score 13;  DB 9;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 98;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         19 GTAGACGGTGCTG 31
              |||||||||||||
Db         16 GTAGACGGTGCTG 4


RESULT 6
US-11-083-784-1558548/c
; Sequence 1558548, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
```

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1558548
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-1558548

Query Match 41.9%; Score 13; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GGAAGTTGAGTAG 22
||||||||||||||
Db 13 GGAAGTTGAGTAG 1

RESULT 7
US-11-101-244-203873/c
; Sequence 203873, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 203873
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-203873

Query Match 38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCGGAAGTTGAG 19
||||||||||||
Db 15 CCGGAAGTTGAG 4

RESULT 8
US-11-101-244-203933/c
; Sequence 203933, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 203933
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-203933

Query Match 38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CCGGAAGTTGAG 19
||||||||||||
Db 15 CCGGAAGTTGAG 4

RESULT 9
US-11-101-244-252961/c
; Sequence 252961, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 252961
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-252961

Query Match 38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 TGAGTAGACGGT 27
||||||||||||
Db 17 TGAGTAGACGGT 6

RESULT 10
US-11-101-244-289277
; Sequence 289277, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela

; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 289277
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-289277

Query Match 38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 75.0%; Pred. No. 3.6e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CGGAAGTTGAGT 20
||||||::|||:
Db 4 CGGAAGUUGAGU 15

RESULT 11
US-11-101-244-301698
; Sequence 301698, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 301698
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-301698

Query Match 38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCACCGGAAGTT 16
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Db 8 CCACCGGAAGUU 19

RESULT 12
US-11-101-244-730807
; Sequence 730807, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 730807
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-730807

Query Match 38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 91.7%; Pred. No. 3.6e+02;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GCCACCGGAAGT 15
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Db 8 GCCACCGGAAGU 19

RESULT 13
US-11-101-244-734540
; Sequence 734540, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 734540
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-734540

Query Match 38.7%; Score 12; DB 8; Length 19;
Best Local Similarity 75.0%; Pred. No. 3.6e+02;
Matches 9; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 12 AAGTTGAGTAGA 23
|||::|||:|||
Db 2 AAGUUGAGUAGA 13

RESULT 14
US-11-101-244-769352/c
; Sequence 769352, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William

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;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 769352
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-769352

  Query Match             38.7%;  Score 12;  DB 8;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGAAGTTGAGTA 21
               ||||||||||||
Db         13 GGAAGTTGAGTA 2


RESULT 15
US-11-101-244-769426/c
; Sequence 769426, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 769426
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-769426

  Query Match             38.7%;  Score 12;  DB 8;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+02;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GGAAGTTGAGTA 21
               ||||||||||||
Db         12 GGAAGTTGAGTA 1


Search completed: December 12, 2005, 06:41:02
Job time : 119 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 02:07:32 ; Search time 1693 Seconds
(without alignments)
805.814 Million cell updates/sec

Title: US-10-688-489-74
Perfect score: 24
Sequence: 1 tccgagacggttctgagggcttac 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 220922

Minimum DB seq length: 22
Maximum DB seq length: 24

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
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10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	12	50.0	22	6	AR568140	AR568140 Sequence
	2	11	45.8	22	6	BD103599	BD103599 Mood diso
	3	11	45.8	22	6	AX021007	AX021007 Sequence
c	4	11	45.8	23	6	AR487560	AR487560 Sequence
	5	10	41.7	22	6	A64826	A64826 Sequence 2
	6	10	41.7	22	6	BD182575	BD182575 Gene tran
c	7	10	41.7	22	6	CS110845	CS110845 Sequence
c	8	10	41.7	22	6	CS111631	CS111631 Sequence
c	9	10	41.7	22	6	AR219168	AR219168 Sequence
c	10	10	41.7	22	6	AX657380	AX657380 Sequence
c	11	10	41.7	23	6	AR090696	AR090696 Sequence
c	12	10	41.7	23	6	AR091566	AR091566 Sequence
	13	10	41.7	23	6	AR154050	AR154050 Sequence
	14	10	41.7	23	6	BD130156	BD130156 Material
c	15	10	41.7	23	6	BD134794	BD134794 Method an
	16	10	41.7	23	6	CQ890765	CQ890765 Sequence
	17	10	41.7	23	6	CQ897305	CQ897305 Sequence
	18	10	41.7	23	6	CQ898454	CQ898454 Sequence
c	19	10	41.7	23	6	CQ967582	CQ967582 Sequence
c	20	10	41.7	23	6	AR197731	AR197731 Sequence
c	21	10	41.7	23	6	AR221816	AR221816 Sequence
c	22	10	41.7	23	6	AR259885	AR259885 Sequence
	23	10	41.7	23	6	AR565274	AR565274 Sequence
c	24	10	41.7	23	6	AR584243	AR584243 Sequence
	25	10	41.7	24	6	A57695	A57695 Sequence 5
	26	10	41.7	24	6	A76942	A76942 Sequence 4
c	27	10	41.7	24	6	AR084744	AR084744 Sequence
	28	10	41.7	24	6	CS083207	CS083207 Sequence
	29	10	41.7	24	6	AR239100	AR239100 Sequence
c	30	10	41.7	24	6	AR360527	AR360527 Sequence
c	31	10	41.7	24	6	AR563493	AR563493 Sequence
c	32	10	41.7	24	6	AR581468	AR581468 Sequence
	33	10	41.7	24	6	AX055394	AX055394 Sequence
	34	10	41.7	24	6	AX077055	AX077055 Sequence
	35	10	41.7	24	6	AX080779	AX080779 Sequence
	36	10	41.7	24	6	AX278902	AX278902 Sequence
c	37	10	41.7	24	6	AX289492	AX289492 Sequence
c	38	10	41.7	24	6	AX291060	AX291060 Sequence
c	39	10	41.7	24	6	AX291739	AX291739 Sequence
	40	10	41.7	24	6	AX447095	AX447095 Sequence
c	41	10	41.7	24	6	AX795373	AX795373 Sequence
	42	9	37.5	22	6	AR017548	AR017548 Sequence
c	43	9	37.5	22	6	AR117174	AR117174 Sequence
c	44	9	37.5	22	6	AR119281	AR119281 Sequence
c	45	9	37.5	22	6	AR136780	AR136780 Sequence

ALIGNMENTS

RESULT 1
AR568140/c
LOCUS AR568140 22 bp DNA linear PAT 08-OCT-2004
DEFINITION Sequence 65 from patent US 6781028.
ACCESSION AR568140
VERSION AR568140.1 GI:53986427
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Costa,M.R., Doberstein,S.K., Elson,S.L., Ferguson,K.C. and Homburger,S.A.
TITLE Animal models and methods for analysis of lipid metabolism and screening of pharmaceutical and pesticidal agents that modulate lipid metabolism
JOURNAL Patent: US 6781028-A 65 24-AUG-2004;
Exelixis, Inc.; South San Francisco, CA
FEATURES Location/Qualifiers
source 1. .22
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 50.0%; Score 12; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 GTTCTGAGGGCT 21
||||||||||||
Db 15 GTTCTGAGGGCT 4

RESULT 2
BD103599
LOCUS BD103599 22 bp DNA linear PAT 27-AUG-2002
DEFINITION Mood disorder gene.
ACCESSION BD103599
VERSION BD103599.1 GI:22649173
KEYWORDS JP 2001526897-A/13.
SOURCE Homo sapiens (human)

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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Broeckhoven,C.V., Raeymaekers,P. and Favero,J.D.
  TITLE     Mood disorder gene
  JOURNAL   Patent: JP 2001526897-A 13 25-DEC-2001;
            VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECHNOLOGIE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001526897-A/13
            PD   25-DEC-2001
            PF   17-DEC-1998 JP 2000525561
            PR   18-DEC-1997 GB    9726804.9
            PI   CHRISTINE VAN BROECKHOVEN,PETER RAEYMAEKERS,JURGEN DEL FAVERO
            PC   C12N15/09,A01K67/027,A61K38/00,A61P25/22,A61P25/24,C07K14/47,
            PC   C12N5/10,
            PC   C12Q1/02,C12Q1/68,C12N15/00,A61K37/02,C12N5/00 CC   Mood
            disorder gene
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             45.8%;  Score 11;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 ACGGTTCTGAG 17
              ||||||||||
Db          6 ACGGTTCTGAG 16


RESULT 3
AX021007
LOCUS       AX021007                  22 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 13 from Patent WO9932643.
ACCESSION   AX021007
VERSION     AX021007.1  GI:10044670
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Del-Favero,J., Raeymaekers,P. and Van Broeckhoven,C.
  TITLE     Mood disorder gene
  JOURNAL   Patent: WO 9932643-A 13 01-JUL-1999;
            BROECKHOVEN CHRISTINE VAN (BE); DEL FAVERO JURGEN (BE); RAEYMAEKERS
            PETER (BE); VLAAMS INTERUNIV INST BIOTECH (BE)
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             45.8%;  Score 11;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 ACGGTTCTGAG 17
              ||||||||||
Db          6 ACGGTTCTGAG 16


RESULT 4
AR487560/c
LOCUS       AR487560                  23 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 10 from patent US 6706505.
ACCESSION   AR487560
VERSION     AR487560.1  GI:47252810
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Han,H.-Q. and Kwak,K.
  TITLE     Human E3.alpha. ubiquitin ligase family
  JOURNAL   Patent: US 6706505-A 10 16-MAR-2004;
            Amgen Inc; Thousand Oaks, CA
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="unknown"
                      /mol_type="genomic DNA"
ORIGIN

  Query Match             45.8%;  Score 11;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 TTCTGAGGGCT 21
               ||||||||||
Db          23 TTCTGAGGGCT 13


RESULT 5
A64826
LOCUS       A64826                    22 bp    DNA     linear   PAT 29-MAR-1999
DEFINITION  Sequence 2 from Patent WO9730178.
ACCESSION   A64826
VERSION     A64826.1  GI:4530817
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified sequences.
REFERENCE   1
  AUTHORS   Neri,C., Cann,H.M. and Cohen,D.
  TITLE     DIAGNOSING TRINUCLEOTIDE REPEAT DISEASES AND GENES INVOLVED THEREIN
  JOURNAL   Patent: WO 9730178-A 2 21-AUG-1997;
            FONDATION JEAN DAUSSET CEPH (FR)
COMMENT     Other publication FR 2745007 19970822.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="unidentified"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32644"
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                      GENETICS"
ORIGIN

  Query Match             41.7%;  Score 10;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 CTGAGGGCTT 22
               ||||||||||
Db           4 CTGAGGGCTT 13


RESULT 6
BD182575
LOCUS       BD182575                  22 bp    DNA     linear   PAT 15-MAY-2003
DEFINITION  Gene transfer of angiogenesis factor into dermatosis.
ACCESSION   BD182575
VERSION     BD182575.1  GI:30793540
KEYWORDS    WO 02089854-A/10.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
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            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Morishita,R., Nakanishi,K., Kaneda,Y. and Kotani,H.
  TITLE     Gene transfer of angiogenesis factor into dermatosis
  JOURNAL   Patent: WO 02089854-A 10 14-NOV-2002;
            ANGES MG INC,RYUICHI MORISHITA,KUNIAKI NAKANISHI,YASUFUMI KANEDA,
            HITOSHI KOTANI
COMMENT     OS   Artificial Sequence
            PN   WO 02089854-A/10
            PD   14-NOV-2002
            PF   09-MAY-2002 WO 2002JP004529
            PR   09-MAY-2001 JP 01P   139373
            PI   RYUICHI MORISHITA,KUNIAKI NAKANISHI,YASUFUMI KANEDA,HITOSHI
            PI   KOTANI
            PC   A61K48/00,A61K38/22,A61P17/02,A61P17/14
            CC   Description of Artificial Sequence:an artificially synthesized

            CC            primer
            CC   sequence
            FH   Key             Location/Qualifiers
            FT   source          1. .22
            FT                   /organism='Artificial Sequence'.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="synthetic construct"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32630"
ORIGIN

  Query Match             41.7%;  Score 10;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGGCT 21
              ||||||||||
Db         12 TCTGAGGGCT 21


RESULT 7
CS110845/c
LOCUS       CS110845                  22 bp    DNA     linear   PAT 22-JUN-2005
DEFINITION  Sequence 88 from Patent WO2005052161.
ACCESSION   CS110845
VERSION     CS110845.1  GI:68148949
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jones,B.E., Kolkman,M., Leeflang,C., Poulose,A.J., Shaw,A., van der
            Kleij,W.A. and van Marrewijk,L.(.
  TITLE     Serine proteases, nucleic acids encoding serine enzymes and vectors
            and host cells incorporating same
  JOURNAL   Patent: WO 2005052161-A 88 09-JUN-2005;
            Genencor International, Inc. (US)
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="primer"
ORIGIN

  Query Match             41.7%;  Score 10;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGAGACGGT 11
              ||||||||||
Db         11 CCGAGACGGT 2


RESULT 8
CS111631/c
LOCUS       CS111631                  22 bp    DNA     linear   PAT 22-JUN-2005
DEFINITION  Sequence 88 from Patent WO2005052146.
ACCESSION   CS111631
VERSION     CS111631.1  GI:68149609
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Jones,B.E., Kolkman,M., Leeflang,C., Oh,H., Poulose,A.J.,
            Sadlowski,E.S., Shaw,A., van der Kleij,W.A. and van Marrewijk,L.(.
  TITLE     Serine proteases, nucleic acids encoding serine enzymes and vectors
            and host cells incorporating same
  JOURNAL   Patent: WO 2005052146-A 88 09-JUN-2005;
            Genencor International, Inc. (US); The Procter & Gamble Company
            (US)
FEATURES              Location/Qualifiers
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                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
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                      /note="primer"
ORIGIN

  Query Match             41.7%;  Score 10;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGAGACGGT 11
              ||||||||||
Db         11 CCGAGACGGT 2


RESULT 9
AR219168/c
LOCUS       AR219168                  22 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 10 from patent US 6420136.
ACCESSION   AR219168
VERSION     AR219168.1  GI:23320102
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Riabowol,K.T., Garkavtsev,I. and Gudkov,A.
  TITLE     Method of modulating p53 activity
  JOURNAL   Patent: US 6420136-A 10 16-JUL-2002;
            University Technologies International, Inc. and Board of Trustees
            of the University of Illinois; Calgary;
            CAX;
FEATURES              Location/Qualifiers
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                      /mol_type="genomic DNA"
ORIGIN

  Query Match             41.7%;  Score 10;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 GAGGGCTTAC 24
              ||||||||||
Db         19 GAGGGCTTAC 10


RESULT 10
AX657380/c
LOCUS       AX657380                  22 bp    DNA     linear   PAT 22-MAR-2003
DEFINITION  Sequence 93 from Patent WO02100896.
ACCESSION   AX657380
VERSION     AX657380.1  GI:29160120
KEYWORDS    .
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SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   dalla Venezia,N.L., Magnard,C.M., Lenoir,G.M. and
            Sinilnikova-Erard,O.
  TITLE     Method for diagnosing cancer susceptibility
  JOURNAL   Patent: WO 02100896-A 93 19-DEC-2002;
            CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (FR);
            UNIVERSITE CLAUDE BERNARD - LYON 1 (FR)
FEATURES             Location/Qualifiers
     source          1. .22
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                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match             41.7%;  Score 10;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTCTGAGGG 19
              ||||||||||
Db         14 GTTCTGAGGG 5


RESULT 11
AR090696/c
LOCUS       AR090696                  23 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 816 from patent US 5994076.
ACCESSION   AR090696
VERSION     AR090696.1  GI:10017451
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Chenchik,A., Jokhadze,G. and Bibilashvilli,R.
  TITLE     Methods of assaying differential expression
  JOURNAL   Patent: US 5994076-A 816 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             41.7%;  Score 10;  DB 6;  Length 23;
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  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 AGACGGTTCT 14
              ||||||||||
Db         19 AGACGGTTCT 10


RESULT 12
AR091566/c
LOCUS       AR091566                  23 bp    DNA     linear   PAT 07-SEP-2000
DEFINITION  Sequence 19 from patent US 5994136.
ACCESSION   AR091566
VERSION     AR091566.1  GI:10018321
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Naldini,L., Dull,T., Farson,D.A. and Witt,R.
  TITLE     Method and means for producing high titer, safe, recombinant
            lentivirus vectors
  JOURNAL   Patent: US 5994136-A 19 30-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             41.7%;  Score 10;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGGCT 21
              ||||||||||
Db         21 TCTGAGGGCT 12


RESULT 13
AR154050
LOCUS       AR154050                  23 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 100 from patent US 6238863.
ACCESSION   AR154050
VERSION     AR154050.1  GI:15122103
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Schumm,J.W. and Bacher,J.W.
  TITLE     Materials and methods for indentifying and analyzing intermediate
            tandem repeat DNA markers
  JOURNAL   Patent: US 6238863-A 100 29-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             41.7%;  Score 10;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CTGAGGGCTT 22
              ||||||||||
Db         11 CTGAGGGCTT 20


RESULT 14
BD130156
LOCUS       BD130156                  23 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Material and method for specifying and analyzing medium-size tandem
            repeat DNA marker.
ACCESSION   BD130156
VERSION     BD130156.1  GI:23225101
KEYWORDS    JP 2002502606-A/100.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Schumm,J.W. and Bacher,J.W.
  TITLE     Material and method for specifying and analyzing medium-size tandem
            repeat DNA marker
  JOURNAL   Patent: JP 2002502606-A 100 29-JAN-2002;
            PROMEGA CORP
COMMENT     OS   Unidentified
            PN   JP 2002502606-A/100
            PD   29-JAN-2002
            PF   04-FEB-1999 JP 2000530608
            PR   04-FEB-1998 US    09/018584
            PI   JAMES W SCHUMM,JEFFREY W BACHER
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Material and method for specifying and analyzing medium-size
            CC            tandem repeat
            CC   DNA marker
            FH   Key             Location/Qualifiers
```

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            FT   source          1. .23
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             41.7%;  Score 10;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CTGAGGGCTT 22
              ||||||||||
Db         11 CTGAGGGCTT 20


RESULT 15
BD134794/c
LOCUS       BD134794                 23 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Method and means of constructing safe and high-titer recombinant
            lentivirus vector.
ACCESSION   BD134794
VERSION     BD134794.1  GI:23229739
KEYWORDS    JP 2002508184-A/19.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Nardini,L., Dall,T., Ferson,D.A. and Wit,R.
  TITLE     Method and means of constructing safe and high-titer recombinant
            lentivirus vector
  JOURNAL   Patent: JP 2002508184-A 19 19-MAR-2002;
            CELL GENESYS INC
COMMENT     OS   Unidentified
            PN   JP 2002508184-A/19
            PD   19-MAR-2002
            PF   11-DEC-1998 JP 2000539150
            PR   12-DEC-1997 US    08/989394
            PI   LUIGI NARDINI,THOMAS DALL,DEBORAH A FERSON,ROCHEL WIT PC
            C12N15/09,C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Method and means of constructing safe and high-titer  CC
            recombinant
            CC   lentivirus vector
            FH   Key             Location/Qualifiers
            FT   source          1. .23
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             41.7%;  Score 10;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+05;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGGCT 21
              ||||||||||
Db         21 TCTGAGGGCT 12


Search completed: December 12, 2005, 02:56:11
Job time : 1696 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 00:33:47 ; Search time 268 Seconds
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Title: US-10-688-489-74
Perfect score: 24
Sequence: 1 tccgagacggttctgagggcttac 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 442420

Minimum DB seq length: 22
Maximum DB seq length: 24

Post-processing: Listing first 45 summaries

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1: geneseqn1980s:*
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13: geneseqn2004bs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24	100.0	24	12	ADN36752	Adn36752 West Nile
	2	24	100.0	24	12	ADN36753	Adn36753 West Nile
	3	23	95.8	23	12	ADN36754	Adn36754 West Nile
	4	22	91.7	22	12	ADN36755	Adn36755 West Nile
	5	21	87.5	23	12	ADN36827	Adn36827 West Nile
	6	11	45.8	22	2	AAX88557	Aax88557 Human chr
	7	11	45.8	22	6	ABQ74548	Abq74548 Human tra
	8	11	45.8	22	12	ADL90000	Adl90000 Gluconoba
c	9	11	45.8	22	13	ADS84984	Ads84984 Human lun
c	10	11	45.8	23	12	ADJ95450	Adj95450 Human Ubi
c	11	11	45.8	23	13	ADS86872	Ads86872 Primer #2
c	12	11	45.8	23	14	ADZ75830	Adz75830 Human E3a
c	13	11	45.8	24	8	AAL51429	Aal51429 Human cyt
	14	10	41.7	22	2	AAT86564	Aat86564 Primer to
	15	10	41.7	22	2	AAX09818	Aax09818 Human bia
c	16	10	41.7	22	2	AAX28696	Aax28696 Nucleotid
c	17	10	41.7	22	4	AAF29770	Aaf29770 Presenili
	18	10	41.7	22	5	AAF24279	Aaf24279 Snrpn tra
	19	10	41.7	22	5	AAS22206	Aas22206 Human COL
c	20	10	41.7	22	8	ABZ79406	Abz79406 Acetyl-Co
	21	10	41.7	22	8	ABX72336	Abx72336 Human NOV
	22	10	41.7	22	10	ABZ23694	Abz23694 CoIalpha1
c	23	10	41.7	22	14	ADY54487	Ady54487 Mouse Myb
	24	10	41.7	22	14	ADZ48734	Adz48734 Insulin s
c	25	10	41.7	22	14	AEA79778	Aea79778 ASP gene
c	26	10	41.7	22	14	AEA48271	Aea48271 Primer fo
c	27	10	41.7	23	2	AAQ52195	Aaq52195 Neuroblas
	28	10	41.7	23	2	AAZ27800	Aaz27800 PCR prime
c	29	10	41.7	23	3	AAA11370	Aaa11370 Human gua
	30	10	41.7	23	3	AAZ57979	Aaz57979 DNA-depen
c	31	10	41.7	23	4	AAC86355	Aac86355 Linker us
c	32	10	41.7	23	6	ABK66728	Abk66728 Human gen
c	33	10	41.7	23	12	ADI04100	Adi04100 2-LTR cir
	34	10	41.7	23	13	ADT26038	Adt26038 P2X7R ion
	35	10	41.7	23	13	ADU23866	Adu23866 Human ATP
c	36	10	41.7	23	14	ADV14724	Adv14724 Human adi
	37	10	41.7	24	2	AAT39994	Aat39994 Primer FO
c	38	10	41.7	24	2	AAX26900	Aax26900 PCR prime
c	39	10	41.7	24	3	AAA88061	Aaa88061 Mouse OCT
c	40	10	41.7	24	3	AAA09894	Aaa09894 Mouse OCT
	41	10	41.7	24	4	AAF30079	Aaf30079 Human PRO
	42	10	41.7	24	5	AAC91507	Aac91507 Human PRO
c	43	10	41.7	24	6	AAD31728	Aad31728 Human tum
	44	10	41.7	24	6	ABQ03543	Abq03543 Oligonucl
	45	10	41.7	24	6	ABK28579	Abk28579 Human PRO

ALIGNMENTS

RESULT 1
ADN36752
ID ADN36752 standard; DNA; 24 BP.
XX
AC ADN36752;
XX
DT 15-JUL-2004 (first entry)
XX
DE West Nile virus detection-related oligonucleotide probe SeqID74.
XX
KW hybridisation assay probe; nucleic acid detection;
KW target-complementary sequence; flavivirus; West Nile virus; WNV;
KW RNA virus; infection; meningitis; encephalitis;
KW high throughput screening; probe; ss.
XX
OS West Nile virus.
XX
PN WO2004036190-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-US033639.
XX
PR 16-OCT-2002; 2002US-0418891P.
PR 25-NOV-2002; 2002US-0429006P.
PR 24-FEB-2003; 2003US-0449810P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Linnen JM, Pollner RB, Wu W, Dennis GG, Darby PM;
XX
DR WPI; 2004-389590/36.
XX
PT New hybridization assay probe comprising target-complementary sequence of
PT bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS Claim 27; SEQ ID NO 74; 135pp; English.
XX
CC This invention relates to a novel hybridisation assay probe, for
CC detecting a nucleic acid, which is a probe sequence that comprises a
CC target-complementary sequence of bases, and optionally one or more base
CC sequences that are not complementary to the nucleic acid that is to be

```
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitos, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of an oligonucleotide probe which is related
CC   to the invention.
XX
SQ   Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 24;  DB 12;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.00079;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db          1 TCCGAGACGGTTCTGAGGGCTTAC 24


RESULT 2
ADN36753
ID   ADN36753 standard; DNA; 24 BP.
XX
AC   ADN36753;
XX
DT   15-JUL-2004  (first entry)
XX
DE   West Nile virus detection-related oligonucleotide probe SeqID75.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; probe; ss.
XX
OS   West Nile virus.
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
PR   25-NOV-2002; 2002US-0429006P.
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM,  Pollner RB,  Wu W,  Dennis GG,  Darby PM;
XX
DR   WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Claim 26; SEQ ID NO 75; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitos, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of an oligonucleotide probe which is related
CC   to the invention.
XX
SQ   Sequence 24 BP; 4 A; 6 C; 8 G; 6 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 24;  DB 12;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.00079;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db          1 TCCGAGACGGTTCTGAGGGCTTAC 24


RESULT 3
ADN36754
ID   ADN36754 standard; DNA; 23 BP.
XX
AC   ADN36754;
XX
DT   15-JUL-2004  (first entry)
XX
DE   West Nile virus detection-related oligonucleotide probe SeqID76.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; probe; ss.
XX
OS   West Nile virus.
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
PR   25-NOV-2002; 2002US-0429006P.
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM,  Pollner RB,  Wu W,  Dennis GG,  Darby PM;
XX
DR   WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Claim 26; SEQ ID NO 76; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitos, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of an oligonucleotide probe which is related
CC   to the invention.
XX
SQ   Sequence 23 BP; 4 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

  Query Match             95.8%;  Score 23;  DB 12;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 0.0029;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTA 23
              |||||||||||||||||||||||
Db          1 TCCGAGACGGTTCTGAGGGCTTA 23
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```
RESULT 4
ADN36755
ID   ADN36755 standard; DNA; 22 BP.
XX
AC   ADN36755;
XX
DT   15-JUL-2004  (first entry)
XX
DE   West Nile virus detection-related oligonucleotide probe SeqID77.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; probe; ss.
XX
OS   West Nile virus.
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
PR   25-NOV-2002; 2002US-0429006P.
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM,  Pollner RB,  Wu W,  Dennis GG,  Darby PM;
XX
DR   WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Claim 26; SEQ ID NO 77; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitos, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of an oligonucleotide probe which is related
CC   to the invention.
XX
SQ   Sequence 22 BP; 3 A; 5 C; 8 G; 6 T; 0 U; 0 Other;

  Query Match             91.7%;  Score 22;  DB 12;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTT 22
              ||||||||||||||||||||||
Db          1 TCCGAGACGGTTCTGAGGGCTT 22


RESULT 5
ADN36827
ID   ADN36827 standard; RNA; 23 BP.
XX
AC   ADN36827;
XX
DT   15-JUL-2004  (first entry)
XX
DE   West Nile virus detection-related oligonucleotide probe SeqID149.
XX
KW   hybridisation assay probe; nucleic acid detection;
KW   target-complementary sequence; flavivirus; West Nile virus; WNV;
KW   RNA virus; infection; meningitis; encephalitis;
KW   high throughput screening; probe; ss.
XX
OS   West Nile virus.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .23
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= 2'-methoxyethoxy (2'-MOE) nucleotides"
XX
PN   WO2004036190-A2.
XX
PD   29-APR-2004.
XX
PF   10-OCT-2003; 2003WO-US033639.
XX
PR   16-OCT-2002; 2002US-0418891P.
PR   25-NOV-2002; 2002US-0429006P.
PR   24-FEB-2003; 2003US-0449810P.
XX
PA   (GENP-) GEN-PROBE INC.
XX
PI   Linnen JM,  Pollner RB,  Wu W,  Dennis GG,  Darby PM;
XX
DR   WPI; 2004-389590/36.
XX
PT   New hybridization assay probe comprising target-complementary sequence of
PT   bases, useful in detecting flavivirus, e.g. West Nile virus.
XX
PS   Example 1; SEQ ID NO 149; 135pp; English.
XX
CC   This invention relates to a novel hybridisation assay probe, for
CC   detecting a nucleic acid, which is a probe sequence that comprises a
CC   target-complementary sequence of bases, and optionally one or more base
CC   sequences that are not complementary to the nucleic acid that is to be
CC   detected. The hybridisation assay probes and the kits are useful in
CC   detecting and amplifying a target nucleic acid sequence, for example
CC   flavivirus like West Nile virus, that may be present in a biological
CC   sample. West Nile virus (WNV) is an RNA virus that primarily infects
CC   birds and culex mosquitos, with humans and horses serving as incidental
CC   hosts. Infection of humans can lead to meningitis or encephalitis. The
CC   invention may allow for accurate and efficient high throughput screening.
CC   The present sequence is that of an oligonucleotide probe which is related
CC   to the invention.
XX
SQ   Sequence 23 BP; 5 A; 4 C; 8 G; 0 T; 6 U; 0 Other;

  Query Match             87.5%;  Score 21;  DB 12;  Length 23;
  Best Local Similarity   76.2%;  Pred. No. 0.038;
  Matches   16;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GAGACGGTTCTGAGGGCTTAC 24
              |||||||::|:||||||::||
Db          1 GAGACGGUUCUGAGGGCUUAC 21


RESULT 6
AAX88557
ID   AAX88557 standard; DNA; 22 BP.
XX
AC   AAX88557;
XX
DT   10-SEP-1999  (first entry)
XX
DE   Human chromosome 18q YAC clone amplification primer.
XX
KW   Human chromosome 18q; mood disorder; polymorphic marker; detection;
KW   identification; trinucleotide repeat expansion; schizophrenia;
KW   anxiety disorder; adjustment disorder; personality disorder;
```

KW nucleotide triplet repeat; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9932643-A2.
XX
PD 01-JUL-1999.
XX
PF 17-DEC-1998; 98WO-EP008543.
XX
PR 18-DEC-1997; 97GB-00026804.
XX
PA (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI Van Broeckhoven C, Raeymaekers P, Del-Favero J;
XX
DR WPI; 1999-418934/35.
XX
PT Detecting nucleotide triplet repeats in human chromosome 18q.
XX
PS Claim 29; Fig 15b; 87pp; English.
XX
CC The present invention describes detecting nucleotide triplet repeats in a
CC region of human chromosome 18q disposed between polymorphic markers
CC D18S68 and D18S979 to identify a human gene associated with a mood
CC disorder or related disorder. AAX88542 to AAX88705 represents human
CC chromosome 18q YAC clones and primers corresponding to them, used in the
CC exemplification of the present invention. YAC clones comprising a portion
CC of the region of human chromosome 18q between markers D18S68 and D18S979
CC are used to identify at least one human gene associated with a mood
CC disorder or related disorder. The mood disorder or related disorder, is
CC chosen from the Diagnostic and Statistical Manual of Mental Disorders,
CC version 4 (DSM-IV) taxonomy. This includes mood disorders (296.XX, 300.4,
CC 311, 301, 13, 295.70), schizophrenia and related disorders (295, 297.1,
CC 298.9, 297.3, 298.9), anxiety disorders (300.XX, 309.81, 308.3),
CC adjustment disorders (309.XX) and personality disorders (codes 301.XX).
CC Probes derived from genes associated with the mood disorder or related
CC disorder can be used to detect pathological mutations or genetic
CC variations in patients. The methods, probes and antibodies can be used to
CC determine the susceptibility of an individual to a mood disorder or
CC related disorder. The nucleic acids and proteins of the human gene can be
CC used to treat mood disorders and related disorders
XX
SQ Sequence 22 BP; 5 A; 5 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 45.8%; Score 11; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ACGGTTCTGAG 17
||||||||||||
Db 6 ACGGTTCTGAG 16

RESULT 7
ABQ74548
ID ABQ74548 standard; DNA; 22 BP.
XX
AC ABQ74548;
XX
DT 22-OCT-2002 (first entry)
XX
DE Human transglutaminase-B PCR primer SEQ ID NO:16.
XX
KW Human; transglutaminase; transglutaminase-A; transglutaminase-B; TGMA;
KW TGMB; enzyme; Huntington's disease; neuroprotective; gene therapy;
KW Factor XIII antagonist; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200259265-A2.
XX
PD 01-AUG-2002.
XX
PF 21-DEC-2001; 2001WO-US050405.
XX
PR 21-DEC-2000; 2000US-0257754P.
XX
PA (DECO-) DECODE GENETICS INC.
XX
PI Gurney M, Hannesson HH;
XX
DR WPI; 2002-608452/65.
XX
PT New isolated nucleic acids of transglutaminase (TGM) A and TGMB residing
PT on chromosome 15 and 20, respectively, useful for treating Huntington's
PT disease.
XX
PS Example 2; Page 49; 98pp; English.
XX
CC The present invention describes a human transglutaminase-A (TGMA) which
CC is located to chromosome 15 (more specifically 15q15), and a human
CC transglutaminase-B (TGMB) which is located to chromosome 20. TGMA and
CC TGMB have neuroprotective activity and can be used as Factor XIII
CC antagonist and in gene therapy. Nucleotide sequences encoding TGMA and
CC TGMB can be used as molecular weight markers on Southern gels, and as
CC chromosome markers which are labeled to map related gene positions. They
CC can be used for deriving primers for genetic fingerprinting, for raising
CC anti-polypeptide antibodies using DNA immunisation techniques or as
CC antigen for raising anti-DNA antibodies or for eliciting immune
CC responses. Additionally, the nucleotide sequences are useful for
CC generating TGMs for identifying agents which alter the activity or
CC expression of TGMs, for identifying and expressing recombinant
CC polypeptides for analysis, characterisation or therapeutic use, and as
CC markers for tissues in which the corresponding polypeptide is expressed.
CC A TGM therapeutic agent is useful for treating Huntington's disease. The
CC present sequence represents a PCR primer for human TGMB, which is used in
CC an example from the present invention
XX
SQ Sequence 22 BP; 7 A; 4 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 45.8%; Score 11; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e+04;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TGAGGGCTTAC 24
||||||||||||
Db 4 TGAGGGCTTAC 14

RESULT 8
ADL90000
ID ADL90000 standard; DNA; 22 BP.
XX
AC ADL90000;
XX
DT 20-MAY-2004 (first entry)
XX
DE Gluconobacter oxydans NADH production-related NRF1 gene PCR primer #7.
XX
KW transaldolase activity; glucose-6-phosphate isomerase; NADH production;
KW target substance manufacture; NRF1; PCR; primer; ss.
XX
OS Gluconobacter oxydans.
XX
PN JP2004024140-A.
XX
PD 29-JAN-2004.
XX
PF 26-JUN-2002; 2002JP-00186487.
XX
PR 26-JUN-2002; 2002JP-00186487.
XX
PA (AJIN) AJINOMOTO KK.
XX

```
DR   WPI; 2004-127093/13.
XX
PT   Novel protein having transaldolase activity or glucose-6-phosphate
PT   isomerase activity, useful for producing a target substance e.g.,
PT   xylitol.
XX
PS   Example 5; SEQ ID NO 12; 89pp; Japanese.
XX
CC   The invention comprises the amino acid and coding sequences of
CC   Gluconobacter oxydans proteins which possess transaldolase activity
CC   and/or glucose-6-phosphate isomerase activity. The DNA and protein
CC   sequences of the invention are involved in the production of NADH. The
CC   DNA and protein sequences of the invention are useful for manufacturing a
CC   target substance. The present DNA sequence represents a PCR primer that
CC   was used in an example of the invention.
XX
SQ   Sequence 22 BP; 5 A; 8 C; 6 G; 3 T; 0 U; 0 Other;

  Query Match             45.8%;  Score 11;  DB 12;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 CCGAGACGGTT 12
              ||||||||||
Db          6 CCGAGACGGTT 16


RESULT 9
ADS84984/c
ID   ADS84984 standard; DNA; 22 BP.
XX
AC   ADS84984;
XX
DT   30-DEC-2004  (first entry)
XX
DE   Human lung cancer-specific gene L984P Taqman probe, SEQ ID 20.
XX
KW   Human; cancer; lung cancer; L984P; probe; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "Labelled with FAM"
FT   modified_base   22
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Labelled with TAMRA"
XX
PN   WO2004084804-A2.
XX
PD   07-OCT-2004.
XX
PF   10-MAR-2004; 2004WO-US007451.
XX
PR   24-MAR-2003; 2003US-0457261P.
PR   15-SEP-2003; 2003US-0502995P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Zehentner-Wilkinson BK,  Hayes DCJ,  Houghton RL;
XX
DR   WPI; 2004-737247/72.
XX
PT   Detecting the presence of a cancer cell in a patient by contacting the
PT   sample with two or more oligonucleotide pairs specific for independent
PT   and unrelated polynucleotide sequences and detecting the amplified
PT   polynucleotides.
XX
PS   Example 1; SEQ ID NO 20; 50pp; English.
XX
CC   The present invention relates to a method for detecting the presence of a
CC   cancer cell in a patient. The method comprises: contacting a biological
CC   sample obtained from a patient with two or more PCR primers for a lung
CC   cancer-specific protein polynucleotide; amplifying the polynucleotides;
CC   and detecting the amplified polynucleotides, where the presence of the
CC   amplified polynucleotides indicates the presence of lung cancer cells in
CC   the patient. The method is useful in detecting the presence of a cancer
CC   cell, preferably lung cancer cell in a patient. The present sequence is a
CC   probe for one such lung cancer-specific gene protein used in the method
CC   of the invention.
XX
SQ   Sequence 22 BP; 5 A; 11 C; 5 G; 1 T; 0 U; 0 Other;

  Query Match             45.8%;  Score 11;  DB 13;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 GGTTCTGAGGG 19
              ||||||||||
Db         22 GGTTCTGAGGG 12


RESULT 10
ADJ95450/c
ID   ADJ95450 standard; DNA; 23 BP.
XX
AC   ADJ95450;
XX
DT   03-JUN-2004  (first entry)
XX
DE   Human Ubiquitin ligase E3alpha I PCR primer #4.
XX
KW   Human; ss; PCR; ubiquitin ligase; E3alpha I;
KW   ubiquitin-proteosome pathway; gene therapy; vaccine; muscular atrophy;
KW   cachexia; catabolic disorders; cancer cachexia; renal cachexia;
KW   inflammatory cachexia; muscle wasting disorder; metabolic acidosis;
KW   uremia; burn; hyperthyroidism; Cushing's syndrome; fasting;
KW   denervation atrophy; diabetes mellitus; sepsis; AIDS wasting syndrome;
KW   primer.
XX
OS   Homo sapiens.
XX
PN   US6706505-B1.
XX
PD   16-MAR-2004.
XX
PF   28-NOV-2000; 2000US-00724126.
XX
PR   08-MAR-2000; 2000US-0187911P.
XX
PA   (AMGE-) AMGEN INC.
XX
PI   Han H,  Kwak K;
XX
DR   WPI; 2004-236723/22.
XX
PT   New nucleic acid molecule, useful for preparing a composition for
PT   diagnosing, treating or preventing diseases associated with human
PT   E3approximatelya polypeptide, e.g., muscle atrophy.
XX
PS   Example 1; SEQ ID NO 10; 104pp; English.
XX
CC   The invention relates to a new isolated nucleic acid molecule appearing
CC   as ADJ95441(or its complement) encoding a ubiquitin ligase E3alpha I
CC   protein appearing as ADJ95442. Also included are a vector comprising the
CC   nucleic acid, a host cell comprising the vector, a process of producing a
CC   E3alpha I ubiquitin ligase polypeptide, a composition comprising the
CC   nucleic acid molecule, a reagent comprising a detectably labelled
CC   nucleotide, and a method for determining the presence of a human E3alpha
CC   I ubiquitin ligase nucleic acid in a biological sample. The nucleic acid
CC   molecule is useful for preparing a composition for diagnosing, treating
CC   or preventing diseases associated with human E3alpha I polypeptide, e.g.
CC   muscle atrophy, cachexia, catabolic disorders, cancer cachexia, renal
```

```
CC   cachexia, inflammatory cachexia, muscle wasting disorders associated with
CC   metabolic acidosis, uremia, burns, hyperthyroidism, Cushing's syndrome,
CC   fasting, denervation atrophy, diabetes mellitus, sepsis and AIDS wasting
CC   syndrome. The present sequence is a PCR primer used to isolate cDNA
CC   encoding human E3alpha I.
XX
SQ   Sequence 23 BP; 7 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             45.8%;  Score 11;  DB 12;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TTCTGAGGGCT 21
              ||||||||||
Db         23 TTCTGAGGGCT 13


RESULT 11
ADS86872/c
ID   ADS86872 standard; DNA; 23 BP.
XX
AC   ADS86872;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Primer #2294-37 for PCR of human E3alphaI ubiquitin ligase gene.
XX
KW   Human; E3alpha ubiquitin ligase; huE3alphaI;
KW   ubiquitin-proteasome pathway; chromosome 15 q; rapid muscle wasting;
KW   fasting; metabolic acidosis; muscle degeneration; kidney failure;
KW   renal cachexia; uremia; diabetes mellitus; sepsis; AIDS wasting syndrome;
KW   cancer cachexia; negative nitrogen balance; burn; Cushing's syndrome;
KW   inflammatory cachexia; hyperthyroidism; denervation atrophy;
KW   protein/tissue wasting; energy-protein malnutrition; muscle atrophy;
KW   gene therapy; ss; primer; PCR; primer #2294-37.
XX
OS   Homo sapiens.
XX
PN   US2004185037-A1.
XX
PD   23-SEP-2004.
XX
PF   15-JAN-2004; 2004US-00758672.
XX
PR   08-MAR-2000; 2000US-0187911P.
PR   28-NOV-2000; 2000US-00724126.
XX
PA   (HANH/) HAN H.
PA   (KWAK/) KWAK K.
XX
PI   Han H,  Kwak K;
XX
DR   WPI; 2004-707854/69.
XX
PT   Novel isolated human E3alpha ubiquitin ligase nucleic acid molecule
PT   useful for treating and/or preventing renal cachexia or inflammatory
PT   cachexia.
XX
PS   Example 1; SEQ ID NO 10; 115pp; English.
XX
CC   The present invention relates to new orthologue of human E3alpha
CC   ubiquitin ligase, huE3alphaI and huE3alphaII. Most intracellular proteins
CC   are degraded through the ubiquitin-proteasome pathway. Proteins are
CC   marked for proteasomal degradation by conjugation of ubiquitin to the
CC   protein. Conjugation of the ubiquitin molecule involves the activation by
CC   E1 enzyme, subsequent transfer to E2 enzyme, which serves as a carrier,
CC   and then interacts with a specific E3 ligase family member. E3 ligase
CC   binds to proteins targeted for degradation and catalyses the transfer of
CC   ubiquitin from the E2 carrier enzyme to the target protein. E3 ligase
CC   determines the specificity of the system. The E3alpha family is the main
CC   family of intracellular ligases and is involved in the N-end rule pathway
CC   of protein degradation. E3alpha enzyme binds directly to the primary
CC   destabilising N-terminal amino acid and catalyses ubiquitin conjugation
CC   thereby targeting the protein for degradation. The human E3alpha gene is
CC   located on chromosome 15 q. Increased proteolysis through the ubiquitin-
CC   proteosome pathway has been determined to be a major cause of rapid
CC   muscle wasting including, fasting, metabolic acidosis, muscle
CC   degeneration, kidney failure, renal cachexia, uremia, diabetes mellitus,
CC   sepsis, AIDS wasting syndrome, cancer cachexia, negative nitrogen
CC   balance, burns, Cushing's syndrome, inflammatory cachexia,
CC   hyperthyroidism, denervation atrophy, protein/tissue wasting, and energy-
CC   protein malnutrition. E3alpha plays a role in the overall increase in
CC   ubiquitination that is associated with and may mediate muscle atrophy in
CC   catabolic and other disease states. Treatment may be administered by gene
CC   therapy, cell therapy and antisense therapy methods. The present sequence
CC   is primer #2294-37 for PCR of the huE3alphaI gene including the 5' and 3'
CC   untranslated regions.
XX
SQ   Sequence 23 BP; 7 A; 9 C; 2 G; 5 T; 0 U; 0 Other;

  Query Match             45.8%;  Score 11;  DB 13;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TTCTGAGGGCT 21
              ||||||||||
Db         23 TTCTGAGGGCT 13


RESULT 12
ADZ75830/c
ID   ADZ75830 standard; DNA; 23 BP.
XX
AC   ADZ75830;
XX
DT   14-JUL-2005  (first entry)
XX
DE   Human E3alphaI cloning PCR primer, 2294-37, SEQ ID NO: 10.
XX
KW   Gene therapy; diagnosis; ubiquitin ligase; PCR; primer; ss.
XX
OS   Homo sapiens.
XX
PN   US2005089876-A1.
XX
PD   28-APR-2005.
XX
PF   15-JAN-2004; 2004US-00758636.
XX
PR   08-MAR-2000; 2000US-0187911P.
PR   28-NOV-2000; 2000US-00724126.
XX
PA   (HANH/) HAN H.
PA   (KWAK/) KWAK K.
XX
PI   Han H,  Kwak K;
XX
DR   WPI; 2005-314084/32.
XX
PT   New isolated nucleic acid molecules encoding human E3alpha ubiquitin
PT   ligase polypeptides, useful for diagnosing, preventing or treating
PT   diseases associated with the polypeptides, e.g. conditions involving
PT   muscle atrophy.
XX
PS   Example 1; SEQ ID NO 10; 113pp; English.
XX
CC   The present invention relates to human E3alpha ubiquitin ligase
CC   polypeptides (huE3alphaI and huE3alphaII) and their encoding
CC   polynucleotides. The invention is useful for diagnosing, preventing and
CC   treating diseases associated with huE3alpha polypeptides as well as
CC   methods for identifying modulators of huE3alpha ligase activity. The
CC   invention is also useful in gene therapy. The present sequence is the
CC   human E3alpha ubiquitin ligase I cloning PCR primer.
XX
SQ   Sequence 23 BP; 7 A; 9 C; 2 G; 5 T; 0 U; 0 Other;
```

```
  Query Match             45.8%;  Score 11;  DB 14;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TTCTGAGGGCT 21
              ||||||||||
Db         23 TTCTGAGGGCT 13


RESULT 13
AAL51429/c
ID   AAL51429 standard; DNA; 24 BP.
XX
AC   AAL51429;
XX
DT   03-APR-2003  (first entry)
XX
DE   Human cytoskeleton relative protein 11-33 PCR primer #1.
XX
KW   Human; ss; cytoskeleton relative protein; 11.33; malignant tumour;
KW   haemopathy; HIV; immunological disease; inflammation; PCR; primer.
XX
OS   Homo sapiens.
XX
PN   CN1364801-A.
XX
PD   21-AUG-2002.
XX
PF   10-JAN-2001; 2001CN-00105178.
XX
PR   10-JAN-2001; 2001CN-00105178.
XX
PA   (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2003-000513/01.
XX
PT   New polypeptide-human cytoskeleton relative protein 11.33 and
PT   polynucleotide for encoding such polypeptide.
XX
PS   Example 2; Page 17 (Disclosure); 33pp; Chinese.
XX
CC   The invention comprises the amino acid and coding sequence of the human
CC   cytoskeleton relative protein 11.33. The DNA and protein sequences of the
CC   invention are useful for treating: malignant tumours; haemopathy; HIV
CC   infection; immunological diseases; and inflammations. The present DNA
CC   sequence represents a PCR primer for the human cytoskeleton relative
CC   protein 11.33 coding sequence
XX
SQ   Sequence 24 BP; 7 A; 10 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             45.8%;  Score 11;  DB 8;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1.6e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TTCTGAGGGCT 21
              ||||||||||
Db         15 TTCTGAGGGCT 5


RESULT 14
AAT86564
ID   AAT86564 standard; DNA; 22 BP.
XX
AC   AAT86564;
XX
DT   24-MAR-1998  (first entry)
XX
DE   Primer to amplify clone 2.116 containing DNA enriched in triplet repeats.
XX
KW   Triplet repeat; transcribed DNA; trinucleotide repeat disease;
KW   myotonic dystrophy; Parkinson's disease; PCR; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9730178-A2.
XX
PD   21-AUG-1997.
XX
PF   17-FEB-1997;   97WO-FR000297.
XX
PR   15-FEB-1996;   96FR-00001864.
XX
PA   (DAUS-) FOND DAUSSET-CEPH JEAN.
XX
PI   Neri C,  Cann HM,  Cohen D;
XX
DR   WPI; 1997-425052/39.
XX
PT   New human transcribed DNA sequences enriched in triplet repeats - used
PT   for treating tri:nucleotide repeat diseases or assessing the risk of
PT   their development e.g. myotonic dystrophy, Parkinson's disease, etc.
XX
PS   Claim 5; Page 11; 26pp; French.
XX
CC   PCR primers AAT86563-80 were used to amplify nine specific transcribed
CC   DNAs (sequences not given in the specification), enriched in the triplets
CC   CAG or CTG, and their normal or mutated alleles, or complementary
CC   sequences. Sequence comparison between patient DNA and these specific DNA
CC   sequences is used to assess the risk of development of a trinucleotide
CC   repeat disease, i.e. spinobulbular muscular dystrophy; myotonic dystrophy
CC   ; cerebrospinal ataxia; dentato-rubropallidoluysian atrophy or
CC   Huntington's disease, although many other diseases (e.g, schizophrenia,
CC   autism, Parkinson's disease, obsessive disorders) may also be caused by
CC   such repeats. The presence of additional triplets indicates risk of
CC   disease and the number of extra triplets allows estimation of the age at
CC   which the disease will develop and its severity
XX
SQ   Sequence 22 BP; 4 A; 3 C; 6 G; 9 T; 0 U; 0 Other;

  Query Match             41.7%;  Score 10;  DB 2;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 5.7e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CTGAGGGCTT 22
              ||||||||||
Db          4 CTGAGGGCTT 13


RESULT 15
AAX09818
ID   AAX09818 standard; DNA; 22 BP.
XX
AC   AAX09818;
XX
DT   24-MAR-1999  (first entry)
XX
DE   Human biallelic polymorphic marker downstream primer #124.
XX
KW   Polymorphism; biallelic; human; forensic; paternity testing; disease;
KW   detection; phenotypic typing; characteristic; infection; hereditary;
KW   autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KW   treatment; marker; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9820165-A2.
XX
PD   14-MAY-1998.
XX
PF   05-NOV-1997;   97WO-US020313.
XX
PR   06-NOV-1996;   96US-0030455P.
```

XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Lander ES, Wang D, Hudson T;
XX
DR WPI; 1998-286974/25.
XX
PT New isolated nucleic acid segments from the human genome - used for
PT determining polymorphic forms for use in e.g. forensics, paternity
PT testing or phenotypic typing for disease.
XX
PS Claim 16; Page 60; 310pp; English.
XX
CC AAX09121-X10268 are allele-specific oligonucleotide primers used in the
CC isolation of various biallelic polymorphic markers found in the human
CC genome (represented in AAX10269-X12937). These primers can be used in a
CC method for determining polymorphic forms in an individual for use in e.g.
CC forensics, paternity testing or for phenotypic typing for diseases such
CC as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular
CC dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial
CC hypercholesterolemia, polycystic kidney disease, hereditary
CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,
CC autoimmune diseases, inflammation, cancer, diseases of the nervous
CC system, infection by pathogenic microorganisms, and characteristics such
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,
CC endurance, fertility, and susceptibility or receptivity to particular
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid
CC segments can also be used to produce medicaments for the treatment or
CC prophylaxis of such diseases
XX
SQ Sequence 22 BP; 9 A; 1 C; 8 G; 4 T; 0 U; 0 Other;

Query Match 41.7%; Score 10; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGTTCTGAGG 18
||||||||||
Db 2 GGTTCTGAGG 11

Search completed: December 12, 2005, 02:27:51
Job time : 271 secs

OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 02:07:58 ; Search time 1927 Seconds
(without alignments)
582.714 Million cell updates/sec

Title: US-10-688-489-74
Perfect score: 24
Sequence: 1 tccgagacggttctgagggcttac 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9906

Minimum DB seq length: 22
Maximum DB seq length: 24

Post-processing: Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9	37.5	24	6	CB843231	CB843231 M15E-4025
c 2	8	33.3	22	1	AA938474	AA938474 oo56h02.s
3	8	33.3	22	1	AW249729	AW249729 2819657.3
4	8	33.3	22	9	AZ476175	AZ476175 1M0294E14
5	8	33.3	22	9	AZ788615	AZ788615 2M0035F19
c 6	8	33.3	22	9	AZ809838	AZ809838 2M0074G04
7	8	33.3	22	10	AG203045	AG203045 Pan trogl
8	8	33.3	22	11	TA207D04P	AL476704 T. brucei
9	8	33.3	22	11	TA294D03P	AL485077 T. brucei
10	8	33.3	22	11	TA314H07Q	AL489914 T. brucei
11	8	33.3	23	7	CO778596	CO778596 BL004B_B0
c 12	8	33.3	23	9	AZ797023	AZ797023 2M0053F06
c 13	8	33.3	23	10	AG193857	AG193857 Pan trogl
14	8	33.3	23	11	TA201E03Q	AL477466 T. brucei
15	8	33.3	24	9	AZ784263	AZ784263 2M0026I19
c 16	7	29.2	22	1	AA926856	AA926856 om07f06.s
17	7	29.2	22	5	BX565934	BX565934 BX565934
18	7	29.2	22	6	CF330336	CF330336 NACL--06-
c 19	7	29.2	22	9	AZ311109	AZ311109 1M0026E21
c 20	7	29.2	22	9	AZ318102	AZ318102 1M0037J11
21	7	29.2	22	9	AZ407386	AZ407386 1M0178K06
c 22	7	29.2	22	9	AZ505531	AZ505531 1M0346F13
c 23	7	29.2	22	9	AZ776605	AZ776605 2M0010I19
24	7	29.2	22	9	AZ806134	AZ806134 2M0068D05
c 25	7	29.2	22	9	AZ861877	AZ861877 2M0168G07
c 26	7	29.2	22	9	BH852180	BH852180 SALK_0742
c 27	7	29.2	22	10	AJ587479	AJ587479 Arabidops
28	7	29.2	22	10	AJ590848	AJ590848 Arabidops
c 29	7	29.2	22	10	CL653644	CL653644 PRI0119a_
30	7	29.2	22	10	CL660428	CL660428 PRI0137a_
31	7	29.2	22	11	TA327G01Q	AL493268 T. brucei
c 32	7	29.2	23	1	AJ651207	AJ651207 AJ651207
33	7	29.2	23	1	AJ801164	AJ801164 AJ801164
34	7	29.2	23	3	BM397206	BM397206 5009-0-3-
35	7	29.2	23	6	CF326961	CF326961 NACL--01-
c 36	7	29.2	23	7	CK812850	CK812850 Rasgsc197
c 37	7	29.2	23	9	AZ380370	AZ380370 1M0136G15
c 38	7	29.2	23	9	AZ475927	AZ475927 1M0294B21
39	7	29.2	23	9	AZ622587	AZ622587 1M0459F02
40	7	29.2	23	9	AZ785027	AZ785027 2M0028H03
c 41	7	29.2	23	9	AZ789956	AZ789956 2M0038L05
42	7	29.2	23	11	TA120H10P	AL462505 T. brucei
43	7	29.2	23	11	TA338E01P	AL493153 T. brucei
c 44	7	29.2	24	1	AU258060	AU258060 AU258060
45	7	29.2	24	1	AU260297	AU260297 AU260297

ALIGNMENTS

RESULT 1
CB843231
LOCUS CB843231 24 bp mRNA linear EST 25-AUG-2004
DEFINITION M15E-4025 MOUSE EMBRYONIC DAY 15.5 EYE Mus musculus cDNA 5', mRNA sequence.
ACCESSION CB843231
VERSION CB843231.2 GI:51550363
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 24)
AUTHORS Yu,J., Farjo,R., MacNee,S.P., Baehr,W., Stambolian,D.E. and Swaroop,A.
TITLE Annotation and analysis of 10,000 expressed sequence tags from developing mouse eye and adult retina
JOURNAL Genome Biol. 4 (10), R65 (2003)
PUBMED 14519200
COMMENT On Sep 1, 2003 this sequence version replaced gi:34374345.
Contact: Swaroop, A.
Department of Ophthalmology and Visual Sciences
Kellogg Eye Center, University of Michigan
540 KEC, 1000 Wall St., Ann Arbor, MI 48105, USA
Tel: 734 615 2246
Fax: 734 647 0228
Email: swaroop@umich.edu.
FEATURES Location/Qualifiers
source 1. .24
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/tissue_type="eye"
/clone_lib="MOUSE EMBRYONIC DAY 15.5 EYE"
/note="Vector: pSPORT1"
ORIGIN

Query Match 37.5%; Score 9; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CGGTTCTGA 16
|||||||||
Db 10 CGGTTCTGA 18

```
RESULT 2
AA938474/c
LOCUS       AA938474                 22 bp    mRNA    linear   EST 30-APR-1998
DEFINITION  oo56h02.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1570227 3'
            similar to TR:Q92555 Q92555 MYELOBLAST KIAA0266. ;, mRNA sequence.
ACCESSION   AA938474
VERSION     AA938474.1  GI:3096513
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1570227"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu5"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     neuroendocrine lung carcinoid, and was then primed with a
                     Not I - oligo(dT) primer. Double-stranded cDNA was ligated
                     to Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector.  Library is normalized. Library was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

  Query Match           33.3%;  Score 8;  DB 1;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 4.5e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 GAGGGCTT 22
              ||||||||
Db         14 GAGGGCTT 7


RESULT 3
AW249729
LOCUS       AW249729                 22 bp    mRNA    linear   EST 07-JAN-2000
DEFINITION  2819657.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819657 3',
            mRNA sequence.
ACCESSION   AW249729
VERSION     AW249729.1  GI:6592722
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: 2819657.5prime
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross_match from University of Washington Genome Center
            PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 11
            contiguous PHRED high quality bases following vector sequence. Very
            Low Quality Sequence: Trace file contained 22 contiguous distinct
            peaks following vector sequence. Polyadenylation: Based upon the
            presence of a XhoI site followed by a run of 14 or more T residues
            at the beginning of the sequence, this cDNA insert was
            polyadenylated.
            Plate: LLCM2  row: C  column: 18
            High quality sequence stop: 11.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2819657"
                     /tissue_type="small cell carcinoma"
                     /cell_line="MGC3"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_7"
                     /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

  Query Match           33.3%;  Score 8;  DB 1;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 4.5e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGAC 8
              ||||||||
Db         10 TCCGAGAC 17


RESULT 4
AZ476175
LOCUS       AZ476175                 22 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0294E14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0294E14 R, genomic survey sequence.
ACCESSION   AZ476175
VERSION     AZ476175.1  GI:10634300
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
```

```
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0294  row: E  column: 14
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0294E14"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             33.3%;  Score 8;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGG 19
              ||||||||
Db         12 TCTGAGGG 19


RESULT 5
AZ788615
LOCUS       AZ788615                 22 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0035F19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0035F19 R, genomic survey sequence.
ACCESSION   AZ788615
VERSION     AZ788615.1  GI:12928595
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0035  row: F  column: 19
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0035F19"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             33.3%;  Score 8;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TGAGGGCT 21
              ||||||||
Db          5 TGAGGGCT 12


RESULT 6
AZ809838/c
LOCUS       AZ809838                 22 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0074G04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0074G04 F, genomic survey sequence.
ACCESSION   AZ809838
VERSION     AZ809838.1  GI:12976504
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
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            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0074  row: G  column: 04
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0074G04"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match            33.3%;  Score 8;  DB 9;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 4.5e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGG 19
               ||||||||
Db          9 TCTGAGGG 2


RESULT 7
AG203045
LOCUS       AG203045                  22 bp    DNA     linear   GSS 06-MAR-2004
DEFINITION  Pan troglodytes DNA, clone: RP43-087A06.T7, genomic survey
            sequence.
ACCESSION   AG203045
VERSION     AG203045.1  GI:45235220
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     BAC end sequences of Library RP-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 22)
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: T7
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-087A06.T7"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match            33.3%;  Score 8;  DB 10;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 4.5e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TGAGGGCT 21
               ||||||||
Db          8 TGAGGGCT 15


RESULT 8
TA207D04P
LOCUS       TA207D04P                 22 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 207d04, forward sequence,
            genomic survey sequence.
ACCESSION   AL476704
VERSION     AL476704.1  GI:11843292
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
```

```
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Trypanosoma brucei"
                      /mol_type="genomic DNA"
                      /strain="TREU927"
                      /db_xref="taxon:5691"
                      /clone="207d04"
ORIGIN

  Query Match          .   33.3%;  Score 8;  DB 11;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 ACGGTTCT 14
              ||||||||
Db          3 ACGGTTCT 10


RESULT 9
TA294D03P
LOCUS       TA294D03P                 22 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 294d03, forward sequence,
            genomic survey sequence.
ACCESSION   AL485077
VERSION     AL485077.1  GI:11852827
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Trypanosoma brucei"
                      /mol_type="genomic DNA"
                      /strain="TREU927"
                      /db_xref="taxon:5691"
                      /clone="294d03"
ORIGIN

  Query Match            33.3%;  Score 8;  DB 11;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 CGAGACGG 10
              ||||||||
Db          5 CGAGACGG 12


RESULT 10
TA314H07Q
LOCUS       TA314H07Q                 22 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 314h07, reverse sequence,
            genomic survey sequence.
ACCESSION   AL489914
VERSION     AL489914.1  GI:11866014
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES              Location/Qualifiers
     source           1. .22
                      /organism="Trypanosoma brucei"
                      /mol_type="genomic DNA"
                      /strain="TREU927"
                      /db_xref="taxon:5691"
                      /clone="314h07"
ORIGIN

  Query Match            33.3%;  Score 8;  DB 11;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TTCTGAGG 18
              ||||||||
Db          3 TTCTGAGG 10


RESULT 11
CO778596
LOCUS       CO778596                  23 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  BL004B_B06 6-Day Axolotl Tail Blastema (6DAxBL) Ambystoma mexicanum
            cDNA 5', similar to hypothetical protein, mRNA sequence.
ACCESSION   CO778596
VERSION     CO778596.1  GI:50994576
KEYWORDS    EST.
SOURCE      Ambystoma mexicanum (axolotl)
  ORGANISM  Ambystoma mexicanum
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
            Ambystoma.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
            Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
  TITLE     An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
            expressed sequence tags from embryonic and regenerating blastema
            cDNA libraries
  JOURNAL   Genome Biol. (2004) In press
COMMENT     Contact: Elly M. Tanaka
            Tanaka Lab
            Max Planck Institute of Molecular Cell Biology and Genetics,
            Dresden
            Pfotenhauerstrasse 108,01307 Dresden, Germany
```

```
            Tel: 0049 351 210 2620
            Fax: 0049 351 210 1489
            Email: tanaka@mpi-cbg.de
            Plate: BL004B  row: 06  column: B
            Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="Ambystoma mexicanum"
                      /mol_type="mRNA"
                      /db_xref="taxon:8296"
                      /tissue_type="Tail Blastema"
                      /cell_type="regenerating tail blastema"
                      /clone_lib="6-Day Axolotl Tail Blastema (6DAxBL)"
                      /note="Vector: pCMVSport6; Site_1: NotI; Site_2: SalI;
                      Unnormalized cDNA plasmid library prepared by Invitrogen.
                      Size fractionated mRNA was polydT primed and cloned into
                      NotI-SalI site of pCMVSport6. Bacterial host is
                      EMDH10B-TONA. Average insert size is 1.67 kB.
                      TAG_LIB=6DAxBL"
ORIGIN

  Query Match             33.3%;  Score 8;  DB 7;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GAGACGGT 11
              ||||||||
Db         14 GAGACGGT 21


RESULT 12
AZ797023/c
LOCUS       AZ797023                 23 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0053F06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0053F06 F, genomic survey sequence.
ACCESSION   AZ797023
VERSION     AZ797023.1  GI:12945674
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0053  row: F  column: 06
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 23.
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="C57BL/6J"
                      /db_xref="taxon:10090"
                      /clone="UUGC2M0053F06"
                      /sex="Male"
                      /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
                      /note="Vector: PWD42nv; Purified genomic DNA from M.
                      musculus C57BL/6J (male) was obtained  from the Jackson
                      Laboratory Mouse DNA Resource
                      (http://www.jax.org/resources/documents/dnares/). The DNA
                      was hydrodynamically sheared by repeated passage through a
                      0.005 inch orifice at constant velocity. The sheared DNA
                      was blunt end-repaired with T4 DNA polymerase and T4
                      polynucleotide kinase. Adaptor oligonucleotides were
                      ligated to the blunt ends in high  molar excess. The
                      adaptored DNA was purified and size-selected for a 9.5 to
                      10.5 kb range using preparative agarose gel
                      electrophoresis. Vector DNA was prepared from a derivative
                      of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                      inducible derivative of plasmid R1. The vector was ligated
                      with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to
                      adaptored vector DNA, and transformed into
                      chemically-competent E. coli XL10-Gold (Stratagene) cells
                      and selected for ampicillin resistance."
ORIGIN

  Query Match             33.3%;  Score 8;  DB 9;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 ACGGTTCT 14
              ||||||||
Db         23 ACGGTTCT 16


RESULT 13
AG193857/c
LOCUS       AG193857                 23 bp    DNA     linear   GSS 06-MAR-2004
DEFINITION  Pan troglodytes DNA, clone: RP43-071F16.T7, genomic survey
            sequence.
ACCESSION   AG193857
VERSION     AG193857.1  GI:45226033
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     BAC end sequences of Library RP-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 23)
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: T7
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES              Location/Qualifiers
     source           1. .23
                      /organism="Pan troglodytes"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9598"
                      /clone="RP43-071F16.T7"
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                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match             33.3%;  Score 8;  DB 10;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TGAGGGCT 21
              ||||||||
Db         18 TGAGGGCT 11


RESULT 14
TA201E03Q
LOCUS       TA201E03Q                23 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 201e03, reverse sequence,
            genomic survey sequence.
ACCESSION   AL477466
VERSION     AL477466.1  GI:11843747
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 23)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb).  The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects.  In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .23
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="201e03"
ORIGIN

  Query Match             33.3%;  Score 8;  DB 11;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         17 GGGCTTAC 24
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Db          3 GGGCTTAC 10


RESULT 15
AZ784263
LOCUS       AZ784263                 24 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0026I19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0026I19 R, genomic survey sequence.
ACCESSION   AZ784263
VERSION     AZ784263.1  GI:12919809
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 24)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0026  row: I  column: 19
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 24.
FEATURES             Location/Qualifiers
     source          1. .24
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0026I19"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             33.3%;  Score 8;  DB 9;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 4.5e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 ACGGTTCT 14
              ||||||||
Db         16 ACGGTTCT 23


Search completed: December 12, 2005, 03:28:25
Job time : 1930 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 02:19:42 ; Search time 93 Seconds
(without alignments)
458.726 Million cell updates/sec

Title: US-10-688-489-74
Perfect score: 24
Sequence: 1 tccgagacggttctgagggcttac 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 107492

Minimum DB seq length: 22
Maximum DB seq length: 24

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	12	50.0	22	3	US-09-332-522E-65	Sequence 65, Appl
c 2	11	45.8	23	3	US-09-724-126A-10	Sequence 10, Appl
3	10	41.7	22	3	US-08-943-731-438	Sequence 438, App
c 4	10	41.7	22	3	US-09-159-871-10	Sequence 10, Appl
c 5	10	41.7	23	2	US-08-859-998-816	Sequence 816, App
c 6	10	41.7	23	2	US-08-989-394-19	Sequence 19, Appl
c 7	10	41.7	23	3	US-09-271-365-19	Sequence 19, Appl
8	10	41.7	23	3	US-09-018-584A-100	Sequence 100, App
c 9	10	41.7	23	3	US-09-225-928-816	Sequence 816, App
c 10	10	41.7	23	3	US-09-604-013A-19	Sequence 19, Appl
c 11	10	41.7	23	3	US-09-225-201B-816	Sequence 816, App
12	10	41.7	23	3	US-09-784-423-100	Sequence 100, App
c 13	10	41.7	23	3	US-10-192-369-3	Sequence 3, Appli
c 14	10	41.7	23	3	US-10-192-085-19	Sequence 19, Appl
c 15	10	41.7	24	2	US-08-691-814B-68	Sequence 68, Appl
16	10	41.7	24	3	US-09-538-709-235	Sequence 235, App
c 17	10	41.7	24	3	US-09-930-803-14	Sequence 14, Appl
c 18	10	41.7	24	3	US-09-521-195B-25	Sequence 25, Appl
c 19	10	41.7	24	3	US-09-798-743-25	Sequence 25, Appl
20	9	37.5	22	2	US-08-139-540-1	Sequence 1, Appli
21	9	37.5	22	2	US-08-197-791-24	Sequence 24, Appl
22	9	37.5	22	2	US-08-634-826-1	Sequence 1, Appli
23	9	37.5	22	3	US-09-115-175-1	Sequence 1, Appli
c 24	9	37.5	22	3	US-09-150-805-6	Sequence 6, Appli
c 25	9	37.5	22	3	US-09-135-021-44	Sequence 44, Appl
c 26	9	37.5	22	3	US-08-978-321-3	Sequence 3, Appli
c 27	9	37.5	22	3	US-08-996-069A-6	Sequence 6, Appli
c 28	9	37.5	22	3	US-09-135-020-46	Sequence 46, Appl
c 29	9	37.5	22	3	US-09-135-010A-46	Sequence 46, Appl
c 30	9	37.5	22	3	US-09-444-871-46	Sequence 46, Appl
c 31	9	37.5	22	3	US-09-597-735-46	Sequence 46, Appl
c 32	9	37.5	22	3	US-09-444-295-46	Sequence 46, Appl
c 33	9	37.5	22	3	US-09-597-732-46	Sequence 46, Appl
34	9	37.5	22	3	US-09-553-690-8	Sequence 8, Appli
c 35	9	37.5	22	3	US-09-597-731-46	Sequence 46, Appl
36	9	37.5	22	3	US-09-755-665-77	Sequence 77, Appl
c 37	9	37.5	22	3	US-09-659-519-10	Sequence 10, Appl
c 38	9	37.5	22	3	US-09-646-561-22	Sequence 22, Appl
c 39	9	37.5	22	3	US-10-037-417-185	Sequence 185, App
40	9	37.5	22	3	US-10-309-814-1	Sequence 1, Appli
41	9	37.5	23	2	US-08-400-580A-10	Sequence 10, Appl
c 42	9	37.5	23	2	US-08-859-998-129	Sequence 129, App
c 43	9	37.5	23	3	US-08-891-789B-24	Sequence 24, Appl
c 44	9	37.5	23	3	US-08-993-674A-80	Sequence 80, Appl
45	9	37.5	23	3	US-09-268-347-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-09-332-522E-65/c
; Sequence 65, Application US/09332522E
; Patent No. 6781028
; GENERAL INFORMATION:
; APPLICANT: Costa, M.
; APPLICANT: Doberstein, S.
; APPLICANT: Elson, S.
; APPLICANT: Ferguson, K.
; APPLICANT: Homberger, S.
; TITLE OF INVENTION: ANIMAL MODELS AND METHODS FOR ANALYSIS OF LIPID METABOLISM AND
; TITLE OF INVENTION: OF PHARMACEUTICAL AND PESTICIDAL AGENTS THAT MODULATE LIPID MET
; FILE REFERENCE: 7326-101, EX99-004
; CURRENT APPLICATION NUMBER: US/09/332,522E
; CURRENT FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-09-332-522E-65

Query Match 50.0%; Score 12; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          10 GTTCTGAGGGCT 21
               ||||||||||||
Db          15 GTTCTGAGGGCT 4
```

RESULT 2
US-09-724-126A-10/c
; Sequence 10, Application US/09724126A
; Patent No. 6706505
; GENERAL INFORMATION:
; APPLICANT: Han, Hui-Quan
; APPLICANT: Kwak, Keith
; TITLE OF INVENTION: Human E3 Alpha Ubiquitin Ligase Family
; FILE REFERENCE: 01017/35966A
; CURRENT APPLICATION NUMBER: US/09/724,126A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/187,211
; PRIOR FILING DATE: 1999-03-01

```
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;    LENGTH: 23
;    TYPE: DNA
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Primer 2294-37
US-09-724-126A-10

  Query Match             45.8%;  Score 11;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.6e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          11 TTCTGAGGGCT 21
               ||||||||||
Db          23 TTCTGAGGGCT 13


RESULT 3
US-08-943-731-438
; Sequence 438, Application US/08943731
; Patent No. 6265157
;  GENERAL INFORMATION:
;    APPLICANT:  PROCKOP, DARWIN J.
;    APPLICANT:  SPOTILA, LORETTA D.
;    APPLICANT:  DELTAS, CONSTANTINOS D.
;    APPLICANT:  SEREDA, LARISA
;    APPLICANT:  LARSON, ANDREA W.
;    APPLICANT:  PACK, MICHAEL
;    APPLICANT:  COLIGE, ALAIN
;    APPLICANT:  EARLY, JAMES
;    APPLICANT:  KORKKO, JARMO
;    APPLICANT:  ALA-KOKKO, LEENA, et al.
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR DETECTING
;    TITLE OF INVENTION:  ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
;    NUMBER OF SEQUENCES:  666
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PANITCH SCHWARZE JACOBS & NADEL, P.C.
;      STREET:  ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
;      STREET:  FLR.
;      CITY:  PHILADELPHIA
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103-7086
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,731
;      FILING DATE:  03-OCT-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/212,322
;      FILING DATE:  14-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/803,628
;      FILING DATE:  03-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DOYLE LEARY Ph.D., KATHRYN
;      REGISTRATION NUMBER:  36,317
;      REFERENCE/DOCKET NUMBER:  9598-27
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-965-1284
;      TELEFAX:  215-567-2991
;      TELEX:  831-494
;  INFORMATION FOR SEQ ID NO:  438:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-943-731-438

  Query Match             41.7%;  Score 10;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           9 GGTTCTGAGG 18
               ||||||||||
Db          11 GGTTCTGAGG 20


RESULT 4
US-09-159-871-10/c
; Sequence 10, Application US/09159871A
; Patent No. 6420136
; GENERAL INFORMATION:
;  APPLICANT:  RIABOWOL, Karl T.
;  TITLE OF INVENTION:  METHOD OF MODULATING P53 ACTIVITY
;  FILE REFERENCE:  028722-181
;  CURRENT APPLICATION NUMBER: US/09/159,871A
;  CURRENT FILING DATE:  1998-09-24
;  PRIOR APPLICATION NUMBER:  US 60/060,138
;  PRIOR FILING DATE:  1997-09-26
;  PRIOR APPLICATION NUMBER:  US 09/006,783
;  PRIOR FILING DATE:  1998-01-14
;  NUMBER OF SEQ ID NOS:  13
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Human
US-09-159-871-10

  Query Match             41.7%;  Score 10;  DB 3;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          15 GAGGGCTTAC 24
               ||||||||||
Db          19 GAGGGCTTAC 10


RESULT 5
US-08-859-998-816/c
; Sequence 816, Application US/08859998
; Patent No. 5994076
;  GENERAL INFORMATION:
;    APPLICANT:  Chenchik, Alex
;    APPLICANT:  Jokhadze, George
;    APPLICANT:  Bibilashvilli, Robert
;    TITLE OF INVENTION:  METHOD OF ASSAYING DIFFERENTIAL
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  1375
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson, P.C.
;      STREET:  2200 Sand Hill Road, Suite 100
;      CITY:  Menlo Park
;      STATE:  CA
;      COUNTRY:  US
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows95
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/859,998
;      FILING DATE:  21-MAY-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
```

```
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Field, Bret E.
;       REGISTRATION NUMBER:  37,620
;       REFERENCE/DOCKET NUMBER:  09096/002001
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-322-5070
;       TELEFAX:  415-854-0875
;   INFORMATION FOR SEQ ID NO:  816:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  23 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
;     FEATURE:
;       OTHER INFORMATION:  oligonucleotide primer
US-08-859-998-816

  Query Match             41.7%;  Score 10;  DB 2;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 AGACGGTTCT 14
              ||||||||||
Db         19 AGACGGTTCT 10


RESULT 6
US-08-989-394-19/c
; Sequence 19, Application US/08989394
; Patent No. 5994136
;  GENERAL INFORMATION:
;    APPLICANT:  Naldini, Luigi
;    APPLICANT:  Dull, Thomas
;    APPLICANT:  Farson, Deborah A.
;    APPLICANT:  Witt, Rochelle
;    TITLE OF INVENTION:  METHOD AND MEANS FOR PRODUCING HIGH
;    TITLE OF INVENTION:  TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SUGHRUE, MION, ZINN, MACPEAK & SEAS
;      STREET:  2100 Pennsylvania Avenue, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/989,394
;      FILING DATE:  12-DEC-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Nakamura, Dean H.
;      REGISTRATION NUMBER:  33,981
;      REFERENCE/DOCKET NUMBER:  A7086
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)293-7060
;      TELEFAX:  (202)293-7860
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-08-989-394-19

  Query Match             41.7%;  Score 10;  DB 2;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGGCT 21
              ||||||||||
Db         21 TCTGAGGGCT 12


RESULT 7
US-09-271-365-19/c
; Sequence 19, Application US/09271365
; Patent No. 6165782
;  GENERAL INFORMATION:
;       APPLICANT: Naldini, Luigi
;                  Dull, Thomas
;                  Farson, Deborah A.
;                  Witt, Rochelle
;       TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
;                           TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
;       NUMBER OF SEQUENCES: 22
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
;            STREET: 2100 Pennsylvania Avenue, N.W.
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20037
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/271,365
;            FILING DATE: 18-Mar-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/989,394
;            FILING DATE: 12-DEC-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Nakamura, Dean H.
;            REGISTRATION NUMBER: 33,981
;            REFERENCE/DOCKET NUMBER: A7086
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (202)293-7060
;            TELEFAX: (202)293-7860
;   INFORMATION FOR SEQ ID NO: 19:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 23 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-271-365-19

  Query Match             41.7%;  Score 10;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGGCT 21
              ||||||||||
Db         21 TCTGAGGGCT 12


RESULT 8
US-09-018-584A-100
; Sequence 100, Application US/09018584A
; Patent No. 6238863
;  GENERAL INFORMATION:
;    APPLICANT:  Schumm, James W.
;    APPLICANT:  Bacher, Jeffery W.
;    TITLE OF INVENTION:  MATERIALS AND METHODS FOR
```

```
;    TITLE OF INVENTION:  IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
;    TITLE OF INVENTION:  REPEAT DNA MARKERS
;    NUMBER OF SEQUENCES:  147
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Promega Corporation
;      STREET:  2800 Woods Hollow Road
;      CITY:  Madison
;      STATE:  Wisconsin
;      COUNTRY:  U.S.A.
;      ZIP:  53711-5399
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette - 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM compatible PC
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  Word 97 (DOS text format)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/018,584A
;      FILING DATE:  04-Feb-1998
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Grady J. Frenchick
;      REGISTRATION NUMBER:  29,018
;      REFERENCE/DOCKET NUMBER:  16026.9180
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (608) 257-3501
;      TELEFAX:  (608) 257-2275
;  INFORMATION FOR SEQ ID NO:  100:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
US-09-018-584A-100

  Query Match             41.7%;  Score 10;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 CTGAGGGCTT 22
               ||||||||||
Db          11 CTGAGGGCTT 20


RESULT 9
US-09-225-928-816/c
; Sequence 816, Application US/09225928
; Patent No. 6352829
;   GENERAL INFORMATION:
;        APPLICANT: Chenchik, Alex
;                   Jokhadze, George
;                   Bibilashvilli, Robert
;        TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                            EXPRESSION
;        NUMBER OF SEQUENCES: 1375
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson, P.C.
;             STREET: 2200 Sand Hill Road, Suite 100
;             CITY: Menlo Park
;             STATE: CA
;             COUNTRY: US
;             ZIP: 94025
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows95
;             SOFTWARE: FastSEQ for Windows Version 2.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/225,928
;             FILING DATE: 05-Jan-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/859,998
;             FILING DATE: 21-MAY-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Field, Bret E.
;             REGISTRATION NUMBER: 37,620
;             REFERENCE/DOCKET NUMBER: 09096/002001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 415-322-5070
;             TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 816:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 23 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        FEATURE:
;             OTHER INFORMATION:  oligonucleotide primer
;        SEQUENCE DESCRIPTION: SEQ ID NO: 816:
US-09-225-928-816

  Query Match             41.7%;  Score 10;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           5 AGACGGTTCT 14
               ||||||||||
Db          19 AGACGGTTCT 10


RESULT 10
US-09-604-013A-19/c
; Sequence 19, Application US/09604013A
; Patent No. 6428953
;   GENERAL INFORMATION:
;        APPLICANT: Naldini, Luigi
;                   Dull, Thomas
;                   Farson, Deborah A.
;                   Witt, Rochelle
;        TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
;                            TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
;             STREET: 2100 Pennsylvania Avenue, N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20037
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/604,013A
;             FILING DATE: 26-Jun-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/271,365
;             FILING DATE: 18-Mar-1999
;             APPLICATION NUMBER: 08/989,394
;             FILING DATE: 12-DEC-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Nakamura, Dean H.
;             REGISTRATION NUMBER: 33,981
;             REFERENCE/DOCKET NUMBER: A7086
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)293-7060
;             TELEFAX: (202)293-7860
;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 23 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
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;           TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-604-013A-19

  Query Match             41.7%;  Score 10;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGGCT 21
              ||||||||||
Db         21 TCTGAGGGCT 12


RESULT 11
US-09-225-201B-816/c
; Sequence 816, Application US/09225201B
; Patent No. 6489455
;   GENERAL INFORMATION:
;       APPLICANT: Chenchik, Alex
;                  Jokhadze, George
;                  Bibilashvilli, Robert
;       TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL
;                           EXPRESSION
;       NUMBER OF SEQUENCES: 1375
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Fish & Richardson, P.C.
;            STREET: 2200 Sand Hill Road, Suite 100
;            CITY: Menlo Park
;            STATE: CA
;            COUNTRY: US
;            ZIP: 94025
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: Windows95
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/225,201B
;            FILING DATE: 05-Jan-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/859,998
;            FILING DATE: 21-MAY-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Field, Bret E.
;            REGISTRATION NUMBER: 37,620
;            REFERENCE/DOCKET NUMBER: 09096/002001
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 415-322-5070
;            TELEFAX: 415-854-0875
;   INFORMATION FOR SEQ ID NO: 816:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 23 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       FEATURE:
;            OTHER INFORMATION:  oligonucleotide primer
;       SEQUENCE DESCRIPTION: SEQ ID NO: 816:
US-09-225-201B-816

  Query Match             41.7%;  Score 10;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 AGACGGTTCT 14
              ||||||||||
Db         19 AGACGGTTCT 10


RESULT 12
US-09-784-423-100
; Sequence 100, Application US/09784423
; Patent No. 6767703
;   GENERAL INFORMATION:
;       APPLICANT: Schumm, James W.
;                  Bacher, Jeffery W.
;       TITLE OF INVENTION: MATERIALS AND METHODS FOR
;                           IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
;                           REPEAT DNA MARKERS
;       NUMBER OF SEQUENCES: 147
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Promega Corporation
;            STREET: 2800 Woods Hollow Road
;            CITY: Madison
;            STATE: Wisconsin
;            COUNTRY: U.S.A.
;            ZIP: 53711-5399
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
;            COMPUTER: IBM compatible PC
;            OPERATING SYSTEM: Windows 95
;            SOFTWARE: Word 97 (DOS text format)
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/784,423
;            FILING DATE: 15-Feb-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/018,584
;            FILING DATE: 04-Feb-1998
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Grady J. Frenchick
;            REGISTRATION NUMBER: 29,018
;            REFERENCE/DOCKET NUMBER: 16026.9180
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (608) 257-3501
;            TELEFAX: (608) 257-2275
;   INFORMATION FOR SEQ ID NO: 100
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 23
;            TYPE: Nucleic Acid
;            STRANDEDNESS: Single
;            TOPOLOGY: Linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 100
US-09-784-423-100

  Query Match             41.7%;  Score 10;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CTGAGGGCTT 22
              ||||||||||
Db         11 CTGAGGGCTT 20


RESULT 13
US-10-192-369-3/c
; Sequence 3, Application US/10192369
; Patent No. 6797464
; GENERAL INFORMATION:
;  APPLICANT: Stevenson, Mario
;  APPLICANT:  Sharkey, Mark
;  TITLE OF INVENTION: DETECTION OF DRUG-RESISTANT HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: 07917-163001
;  CURRENT APPLICATION NUMBER: US/10/192,369
;  CURRENT FILING DATE:  2002-07-10
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
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```
;   OTHER INFORMATION: synthetic probe
US-10-192-369-3

  Query Match             41.7%;  Score 10;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGGCT 21
              ||||||||||
Db         17 TCTGAGGGCT 8


RESULT 14
US-10-192-085-19/c
; Sequence 19, Application US/10192085
; Patent No. 6924144
;   GENERAL INFORMATION:
;        APPLICANT: Naldini, Luigi
;                   Dull, Thomas
;                   Farson, Deborah A.
;                   Witt, Rochelle
;        TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
;                            TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
;             STREET: 2100 Pennsylvania Avenue, N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20037
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/192,085
;             FILING DATE: 10-Jul-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/271,365
;             FILING DATE: 18-Mar-1999
;             APPLICATION NUMBER: 08/989,394
;             FILING DATE: 12-DEC-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Nakamura, Dean H.
;             REGISTRATION NUMBER: 33,981
;             REFERENCE/DOCKET NUMBER: A7086
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)293-7060
;             TELEFAX: (202)293-7860
;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 23 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-192-085-19

  Query Match             41.7%;  Score 10;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGGCT 21
              ||||||||||
Db         21 TCTGAGGGCT 12


RESULT 15
US-08-691-814B-68/c
; Sequence 68, Application US/08691814B
; Patent No. 5981218
;  GENERAL INFORMATION:
;    APPLICANT:  Rio, Marie-Christine
;    APPLICANT:  Tomasetto, Catherine
;    APPLICANT:  Basset, Paul
;    APPLICANT:  Byrne, Jennifer
;    TITLE OF INVENTION:  Isolated Nucleic Acid Molecules Useful
;    TITLE OF INVENTION:  as Leukemia Markers and in Breast Cancer Prognosis
;    NUMBER OF SEQUENCES:  124
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Sterne, Kessler, Goldstein & Fox P.L.L.C.
;      STREET:  1100 New York Ave, NW, Suite 600
;      CITY:  Washington
;      STATE:  DC
;      COUNTRY:  USA
;      ZIP:  20005-3934
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/691,814B
;      FILING DATE:  31-JUL-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/002,183
;      FILING DATE:  09-AUG-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Steffe, Eric K.
;      REGISTRATION NUMBER:  36,688
;      REFERENCE/DOCKET NUMBER:  1383.0090001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-371-2600
;      TELEFAX:  202-371-2543
;  INFORMATION FOR SEQ ID NO:  68:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-691-814B-68

  Query Match             41.7%;  Score 10;  DB 2;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGGCT 21
              ||||||||||
Db         19 TCTGAGGGCT 10


Search completed: December 12, 2005, 03:30:02
Job time : 94 secs
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OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 02:56:14 ; Search time 421 Seconds
(without alignments)
471.413 Million cell updates/sec

Title: US-10-688-489-74
Perfect score: 24
Sequence: 1 tccgagacggttctgagggcttac 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 0

Total number of hits satisfying chosen parameters: 268506

Minimum DB seq length: 22
Maximum DB seq length: 24

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24	100.0	24	8	US-10-688-489-74	Sequence 74, Appl
	2	24	100.0	24	8	US-10-688-489-75	Sequence 75, Appl
	3	23	95.8	23	8	US-10-688-489-76	Sequence 76, Appl
	4	22	91.7	22	8	US-10-688-489-77	Sequence 77, Appl
	5	21	87.5	23	8	US-10-688-489-149	Sequence 149, App
c	6	11	45.8	23	8	US-10-758-672A-10	Sequence 10, Appl
c	7	11	45.8	23	9	US-10-758-636A-10	Sequence 10, Appl
	8	10	41.7	22	7	US-10-114-270-273	Sequence 273, App
	9	10	41.7	22	8	US-10-477-166-10	Sequence 10, Appl
	10	10	41.7	22	9	US-10-887-553A-63	Sequence 63, Appl
	11	10	41.7	23	3	US-09-784-423-100	Sequence 100, App
	12	10	41.7	23	3	US-09-750-410-47	Sequence 47, Appl
c	13	10	41.7	23	5	US-10-192-085-19	Sequence 19, Appl
c	14	10	41.7	23	6	US-10-192-369-3	Sequence 3, Appli
	15	10	41.7	23	8	US-10-712-642-47	Sequence 47, Appl
c	16	10	41.7	23	9	US-10-795-580-3	Sequence 3, Appli
	17	10	41.7	23	9	US-10-825-593-108	Sequence 108, App
c	18	10	41.7	24	3	US-09-798-743A-25	Sequence 25, Appl
	19	10	41.7	24	3	US-09-940-185-3550	Sequence 3550, Ap
	20	10	41.7	24	5	US-10-154-971-5	Sequence 5, Appli
c	21	10	41.7	24	6	US-10-323-463-15	Sequence 15, Appl
c	22	10	41.7	24	6	US-10-403-107-14	Sequence 14, Appl
c	23	10	41.7	24	8	US-10-762-154-25	Sequence 25, Appl
c	24	10	41.7	24	8	US-10-940-500-25	Sequence 25, Appl
c	25	10	41.7	24	9	US-10-257-158A-1254	Sequence 1254, Ap
c	26	10	41.7	24	9	US-10-257-158A-2822	Sequence 2822, Ap
c	27	10	41.7	24	9	US-10-257-158A-3501	Sequence 3501, Ap
	28	9	37.5	22	3	US-09-755-665-77	Sequence 77, Appl
	29	9	37.5	22	3	US-09-796-599-1	Sequence 1, Appli
c	30	9	37.5	22	3	US-09-745-008-25	Sequence 25, Appl
	31	9	37.5	22	3	US-09-729-653-5	Sequence 5, Appli
c	32	9	37.5	22	3	US-09-938-689-52	Sequence 52, Appl
c	33	9	37.5	22	3	US-09-944-161-10	Sequence 10, Appl
	34	9	37.5	22	3	US-09-840-743-77	Sequence 77, Appl
c	35	9	37.5	22	5	US-10-138-316-46	Sequence 46, Appl
	36	9	37.5	22	5	US-10-153-219-26	Sequence 26, Appl
c	37	9	37.5	22	6	US-10-093-626B-56	Sequence 56, Appl
	38	9	37.5	22	6	US-10-309-814-1	Sequence 1, Appli
c	39	9	37.5	22	6	US-10-368-643-46	Sequence 46, Appl
c	40	9	37.5	22	6	US-10-313-669-292	Sequence 292, App
	41	9	37.5	22	7	US-10-203-516A-5	Sequence 5, Appli
c	42	9	37.5	22	7	US-10-203-516A-6	Sequence 6, Appli
c	43	9	37.5	22	7	US-10-037-417-185	Sequence 185, App
c	44	9	37.5	22	7	US-10-380-614-10	Sequence 10, Appl
	45	9	37.5	22	7	US-10-456-848-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-10-688-489-74
; Sequence 74, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 24
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-74

Query Match 100.0%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.3e-05;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24
||||||||||||||||||||||||
Db 1 TCCGAGACGGTTCTGAGGGCTTAC 24

RESULT 2
US-10-688-489-75
; Sequence 75, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen

```
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 75
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-75

  Query Match             100.0%;  Score 24;  DB 8;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-05;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db          1 TCCGAGACGGTTCTGAGGGCTTAC 24


RESULT 3
US-10-688-489-76
; Sequence 76, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 76
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-76

  Query Match             95.8%;  Score 23;  DB 8;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 0.0003;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTA 23
              |||||||||||||||||||||||
Db          1 TCCGAGACGGTTCTGAGGGCTTA 23


RESULT 4
US-10-688-489-77
; Sequence 77, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 77
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-77

  Query Match             91.7%;  Score 22;  DB 8;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 0.0013;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTT 22
              ||||||||||||||||||||||
Db          1 TCCGAGACGGTTCTGAGGGCTT 22


RESULT 5
US-10-688-489-149
; Sequence 149, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
;  APPLICANT: Linnen, Jeffrey M.
;  APPLICANT:  Pollner, Reinhold B.
;  APPLICANT:  Wu, Wen
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 149
;   LENGTH: 23
;   TYPE: RNA
;   ORGANISM: West Nile Virus
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(23)
;   OTHER INFORMATION: 2'-OMe nucleotide analogs
US-10-688-489-149

  Query Match             87.5%;  Score 21;  DB 8;  Length 23;
  Best Local Similarity   76.2%;  Pred. No. 0.0053;
  Matches   16;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GAGACGGTTCTGAGGGCTTAC 24
              |||||||::|:||||||::||
Db          1 GAGACGGUUCUGAGGGCUUAC 21
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```
RESULT 6
US-10-758-672A-10/c
; Sequence 10, Application US/10758672A
; Publication No. US20040185037A1
; GENERAL INFORMATION:
;  APPLICANT: Han, et al.
;  TITLE OF INVENTION: HUMAN E3 ALPHA UBIQUITIN LIGASE FAMILY
;  FILE REFERENCE: 01017/35966B
;  CURRENT APPLICATION NUMBER: US/10/758,672A
;  CURRENT FILING DATE:  2004-01-15
;  PRIOR APPLICATION NUMBER: US 09/724,126
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: US 60/187,911
;  PRIOR FILING DATE: 2000-03-08
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic primer
US-10-758-672A-10

  Query Match             45.8%;  Score 11;  DB 8;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8.2e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TTCTGAGGGCT 21
              ||||||||||| 
Db         23 TTCTGAGGGCT 13


RESULT 7
US-10-758-636A-10/c
; Sequence 10, Application US/10758636A
; Publication No. US20050089876A1
; GENERAL INFORMATION:
;  APPLICANT: Han, et al.
;  TITLE OF INVENTION: HUMAN E3 ALPHA UBIQUITIN LIGASE FAMILY
;  FILE REFERENCE: 01017/35966C
;  CURRENT APPLICATION NUMBER: US/10/758,636A
;  CURRENT FILING DATE:  2004-01-15
;  PRIOR APPLICATION NUMBER: US 09/724,126
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: US 60/187,911
;  PRIOR FILING DATE: 2000-03-08
;  NUMBER OF SEQ ID NOS: 29
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Synthetic primer
US-10-758-636A-10

  Query Match             45.8%;  Score 11;  DB 9;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 8.2e+03;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TTCTGAGGGCT 21
              ||||||||||| 
Db         23 TTCTGAGGGCT 13


RESULT 8
US-10-114-270-273
; Sequence 273, Application US/10114270
; Publication No. US20040030110A1
; GENERAL INFORMATION:
;  APPLICANT: Guo, Xiaojia
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Malyankar, Uriel M.
;  APPLICANT:  Spytek, Kimberly A.
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Liu, Ziaohong
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Li, Li
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Zerhusen, Bryan D.
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Shenoy, Suresh G.
;  APPLICANT:  Pena, Carol E.A.
;  APPLICANT:  Smithson, Glennda
;  APPLICANT:  Burgess, Catherine E.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Shimkets, Richard A.
;  APPLICANT:  Gangolli, Esha A.
;  APPLICANT:  Taupier Jr., Raymond J.
;  APPLICANT:  Casman, Stacie J.
;  APPLICANT:  Ji, Weizhen
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Liete, Mario W.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Edinger, Shlomit R.
;  APPLICANT:  Stone, David J.
;  APPLICANT:  MacDougall, John R.
;  APPLICANT:  Rothenberg, Mark E.
;  TITLE OF INVENTION: No. US20040030110A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-322C
;  CURRENT APPLICATION NUMBER: US/10/114,270
;  CURRENT FILING DATE:  2002-11-27
;  PRIOR APPLICATION NUMBER: 60/281,086
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,136
;  PRIOR FILING DATE: 2001-04-03
;  PRIOR APPLICATION NUMBER: 60/281,863
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/281,906
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/282,020
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: 60/282,930
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/282,934
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: 60/283,512
;  PRIOR FILING DATE: 2001-04-12
;  PRIOR APPLICATION NUMBER: 60/283,710
;  PRIOR FILING DATE: 2001-04-13
;  PRIOR APPLICATION NUMBER: 60/284,234
;  PRIOR FILING DATE: 2001-04-17
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 470
; SEQ ID NO 273
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Forward Primer
US-10-114-270-273

  Query Match             41.7%;  Score 10;  DB 7;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CTGAGGGCTT 22
              |||||||||| 
Db          5 CTGAGGGCTT 14
```

```
RESULT 9
US-10-477-166-10
; Sequence 10, Application US/10477166
; Publication No. US20040234481A1
; GENERAL INFORMATION:
;  APPLICANT: ANGES MG, INC.
;  APPLICANT:  Morishita, Ryuichi
;  APPLICANT:  Nakanishi, Kuniaki
;  APPLICANT:  Kaneda, Yasufumi
;  APPLICANT:  Kotani, Hitoshi
;  TITLE OF INVENTION: GENE TRANSFER OF ANGIOGENIC FACTOR FOR SKIN DISEASE
;  FILE REFERENCE: 6235-67174
;  CURRENT APPLICATION NUMBER: US/10/477,166
;  CURRENT FILING DATE:  2003-11-07
;  PRIOR APPLICATION NUMBER: PCT/JP02/04529
;  PRIOR FILING DATE: 2002-05-09
;  PRIOR APPLICATION NUMBER: JP 2001-139373
;  PRIOR FILING DATE: 2001-05-09
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:an artificially
;   OTHER INFORMATION: synthesized primer sequence
US-10-477-166-10

  Query Match             41.7%;  Score 10;  DB 8;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGGCT 21
              ||||||||||
Db         12 TCTGAGGGCT 21


RESULT 10
US-10-887-553A-63
; Sequence 63, Application US/10887553A
; Publication No. US20050085436A1
; GENERAL INFORMATION:
;  APPLICANT: Garza, Dan
;  APPLICANT:  Li, Hao
;  TITLE OF INVENTION: Method to treat conditions associated
;  TITLE OF INVENTION:  with insulin signalling dysregulation
;  FILE REFERENCE: 4-33262
;  CURRENT APPLICATION NUMBER: US/10/887,553A
;  CURRENT FILING DATE:  2004-07-08
;  PRIOR APPLICATION NUMBER: 60/485,883
;  PRIOR FILING DATE: 2003-08-07
;  NUMBER OF SEQ ID NOS: 1208
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: unknown
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: (1)..(22)
;   OTHER INFORMATION: Reverse primer
US-10-887-553A-63

  Query Match             41.7%;  Score 10;  DB 9;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CGGTTCTGAG 17
              ||||||||||
Db         11 CGGTTCTGAG 20
```

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RESULT 11
US-09-784-423-100
; Sequence 100, Application US/09784423
; Patent No. US20020012924A1
;   GENERAL INFORMATION:
;        APPLICANT: Schumm, James W.
;                   Bacher, Jeffery W.
;        TITLE OF INVENTION: MATERIALS AND METHODS FOR
;                            IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM
;                            REPEAT DNA MARKERS
;        NUMBER OF SEQUENCES: 147
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Promega Corporation
;             STREET: 2800 Woods Hollow Road
;             CITY: Madison
;             STATE: Wisconsin
;             COUNTRY: U.S.A.
;             ZIP: 53711-5399
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb
;             COMPUTER: IBM compatible PC
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: Word 97 (DOS text format)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/784,423
;             FILING DATE: 15-Feb-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/018,584
;             FILING DATE: 04-Feb-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Grady J. Frenchick
;             REGISTRATION NUMBER: 29,018
;             REFERENCE/DOCKET NUMBER: 16026.9180
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (608) 257-3501
;             TELEFAX: (608) 257-2275
;   INFORMATION FOR SEQ ID NO: 100
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 23
;             TYPE: Nucleic Acid
;             STRANDEDNESS: Single
;             TOPOLOGY: Linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 100
US-09-784-423-100

  Query Match             41.7%;  Score 10;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CTGAGGGCTT 22
              ||||||||||
Db         11 CTGAGGGCTT 20


RESULT 12
US-09-750-410-47
; Sequence 47, Application US/09750410
; Publication No. US20030083276A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Gloria C.
;  APPLICANT:  Burgman, Paul W.J.J.
;  TITLE OF INVENTION: USES OF DNA-PK
;  FILE REFERENCE: 1747/55672-A-PCT-US
;  CURRENT APPLICATION NUMBER: US/09/750,410
;  CURRENT FILING DATE:  2000-12-28
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
```

```
;   OTHER INFORMATION: Oligonucleotide Primer
US-09-750-410-47

  Query Match             41.7%;  Score 10;  DB 3;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CTGAGGGCTT 22
              ||||||||||
Db          3 CTGAGGGCTT 12


RESULT 13
US-10-192-085-19/c
; Sequence 19, Application US/10192085
; Publication No. US20020173030A1
;   GENERAL INFORMATION:
;        APPLICANT: Naldini, Luigi
;                   Dull, Thomas
;                   Farson, Deborah A.
;                   Witt, Rochelle
;        TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
;                            TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
;        NUMBER OF SEQUENCES: 22
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
;             STREET: 2100 Pennsylvania Avenue, N.W.
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20037
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/192,085
;             FILING DATE: 10-Jul-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/271,365
;             FILING DATE: 18-Mar-1999
;             APPLICATION NUMBER: 08/989,394
;             FILING DATE: 12-DEC-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Nakamura, Dean H.
;             REGISTRATION NUMBER: 33,981
;             REFERENCE/DOCKET NUMBER: A7086
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (202)293-7060
;             TELEFAX: (202)293-7860
;   INFORMATION FOR SEQ ID NO: 19:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 23 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-192-085-19

  Query Match             41.7%;  Score 10;  DB 5;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGGCT 21
              ||||||||||
Db         21 TCTGAGGGCT 12


RESULT 14
US-10-192-369-3/c
; Sequence 3, Application US/10192369
; Publication No. US20040009124A1
; GENERAL INFORMATION:
;  APPLICANT: Stevenson, Mario
;  APPLICANT:  Sharkey, Mark
;  TITLE OF INVENTION: DETECTION OF DRUG-RESISTANT HUMAN
;  TITLE OF INVENTION:  IMMUNODEFICIENCY VIRUS
;  FILE REFERENCE: 07917-163001
;  CURRENT APPLICATION NUMBER: US/10/192,369
;  CURRENT FILING DATE:  2002-07-10
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic probe
US-10-192-369-3

  Query Match             41.7%;  Score 10;  DB 6;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGGCT 21
              ||||||||||
Db         17 TCTGAGGGCT 8


RESULT 15
US-10-712-642-47
; Sequence 47, Application US/10712642
; Publication No. US20050032726A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Gloria C.
;  APPLICANT:  Burgman, Paul W.J.J.
;  TITLE OF INVENTION: USES OF DNA-PK
;  FILE REFERENCE: 1747/55672-A-PCT-US
;  CURRENT APPLICATION NUMBER: US/10/712,642
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: US/09/750,410
;  PRIOR FILING DATE: 2000-12-28
;  NUMBER OF SEQ ID NOS: 59
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Oligonucleotide Primer
US-10-712-642-47

  Query Match             41.7%;  Score 10;  DB 8;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.4e+04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CTGAGGGCTT 22
              ||||||||||
Db          3 CTGAGGGCTT 12


Search completed: December 12, 2005, 04:27:32
Job time : 422 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 11, 2005, 21:35:42 ; Search time 62.8364 Seconds
(without alignments)
678.930 Million cell updates/sec

Title: US-10-688-489-74
Perfect score: 24
Sequence: 1 tccgagacggttctgagggcttac 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
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9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	16.8	70.0	2799	3	US-08-968-752B-5	Sequence 5, Appli
	2	16.8	70.0	2799	3	US-09-536-224-5	Sequence 5, Appli
	3	16.6	69.2	601	3	US-09-949-016-157466	Sequence 157466,
	4	16.6	69.2	601	3	US-09-949-016-157573	Sequence 157573,
	5	16.6	69.2	601	3	US-09-949-016-198733	Sequence 198733,
	6	16.6	69.2	126176	3	US-09-949-016-16137	Sequence 16137, A
	7	16.6	69.2	126176	3	US-09-949-016-16138	Sequence 16138, A
	8	16.6	69.2	153866	3	US-09-949-016-16919	Sequence 16919, A
	9	16.6	69.2	166698	3	US-09-949-016-16038	Sequence 16038, A
c	10	16.6	69.2	767677	3	US-09-949-016-12147	Sequence 12147, A
c	11	16.6	69.2	767677	3	US-09-949-016-17361	Sequence 17361, A
c	12	16.6	69.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	13	16.6	69.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	14	16.2	67.5	921	3	US-09-107-532A-2264	Sequence 2264, Ap
	15	16.2	67.5	1815	3	US-09-832-496-1	Sequence 1, Appli
	16	16.2	67.5	1815	3	US-09-832-616-1	Sequence 1, Appli
c	17	16.2	67.5	21721	3	US-09-269-939A-41	Sequence 41, Appl
c	18	16.2	67.5	22976	3	US-09-269-939A-19	Sequence 19, Appl
c	19	16.2	67.5	23187	3	US-09-499-522-1	Sequence 1, Appli
	20	16	66.7	522	3	US-09-252-991A-8519	Sequence 8519, Ap
	21	16	66.7	579	3	US-09-270-767-12997	Sequence 12997, A
	22	16	66.7	1113	3	US-09-252-991A-8445	Sequence 8445, Ap
	23	16	66.7	1850	3	US-09-799-451-367	Sequence 367, App
	24	16	66.7	2409	3	US-09-252-991A-8479	Sequence 8479, Ap
c	25	16	66.7	7240	3	US-09-695-795A-1	Sequence 1, Appli
c	26	15.8	65.8	37	2	US-08-199-507B-21	Sequence 21, Appl
c	27	15.8	65.8	37	2	US-08-441-828-21	Sequence 21, Appl
	28	15.8	65.8	601	3	US-09-949-016-192257	Sequence 192257,
	29	15.8	65.8	1621	2	US-08-292-688A-10	Sequence 10, Appl
	30	15.8	65.8	1795	2	US-08-791-849A-12	Sequence 12, Appl
c	31	15.8	65.8	55031	3	US-09-949-016-17389	Sequence 17389, A
c	32	15.8	65.8	90776	3	US-09-949-016-17230	Sequence 17230, A
	33	15.8	65.8	122772	3	US-09-949-016-14132	Sequence 14132, A
	34	15.8	65.8	767677	3	US-09-949-016-12147	Sequence 12147, A
	35	15.8	65.8	767677	3	US-09-949-016-17361	Sequence 17361, A
	36	15.6	65.0	601	3	US-09-949-016-45837	Sequence 45837, A
	37	15.6	65.0	601	3	US-09-949-016-45859	Sequence 45859, A
	38	15.6	65.0	948	3	US-09-489-039A-1034	Sequence 1034, Ap
	39	15.6	65.0	1341	3	US-09-248-796A-6062	Sequence 6062, Ap
c	40	15.6	65.0	2121	3	US-09-902-540-8806	Sequence 8806, Ap
c	41	15.6	65.0	2332	3	US-09-949-016-253	Sequence 253, App
c	42	15.6	65.0	2332	3	US-09-949-016-5522	Sequence 5522, Ap
c	43	15.6	65.0	3595	3	US-09-949-016-408	Sequence 408, App
c	44	15.6	65.0	3607	3	US-09-563-269-17	Sequence 17, Appl
	45	15.6	65.0	3943	3	US-08-506-296B-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-968-752B-5
; Sequence 5, Application US/08968752B
; Patent No. 6043073
; GENERAL INFORMATION:
; APPLICANT: Frohman, Michael A.
; APPLICANT: Morris, Andrew
; TITLE OF INVENTION: No. 6043073el Phospholipase D Polypeptide and
; TITLE OF INVENTION: DNA Sequences
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONYX Pharmaceuticals, Inc.
; STREET: 3031 Research Drive
; CITY: Richmond
; STATE: California
; COUNTRY: USA
; ZIP: 94806
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/968,752B
; FILING DATE: 13-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/025,469
; FILING DATE: 05-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Giotta, Gregory J.
; REGISTRATION NUMBER: 32,028
; REFERENCE/DOCKET NUMBER: ONYX2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-222-9700
; TELEFAX: 510-222-9758
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS

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;      LOCATION:  1..2799
US-08-968-752B-5

  Query Match             70.0%;  Score 16.8;  DB 3;  Length 2799;
  Best Local Similarity   90.0%;  Pred. No. 1.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CCGAGACGGTTCTGAGGGCT 21
              |||||  ||||||||||||
Db        444 CCGAGGAGGTTCTGAGGGCT 463


RESULT 2
US-09-536-224-5
; Sequence 5, Application US/09536224
; Patent No. 6379665
;  GENERAL INFORMATION:
;    APPLICANT:  Frohman, Michael A.
;    APPLICANT:  Morris, Andrew
;    TITLE OF INVENTION:  No. 6379665el Phospholipase D Polypeptide and
;    TITLE OF INVENTION:  DNA Sequences
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ONYX Pharmaceuticals, Inc.
;      STREET:  3031 Research Drive
;      CITY:  Richmond
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94806
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/536,224
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/968,752
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Giotta, Gregory J.
;      REGISTRATION NUMBER:  32,028
;      REFERENCE/DOCKET NUMBER:  ONYX2004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  510-222-9700
;      TELEFAX:  510-222-9758
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2799 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..2799
US-09-536-224-5

  Query Match             70.0%;  Score 16.8;  DB 3;  Length 2799;
  Best Local Similarity   90.0%;  Pred. No. 1.4e+02;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CCGAGACGGTTCTGAGGGCT 21
              |||||  ||||||||||||
Db        444 CCGAGGAGGTTCTGAGGGCT 463


RESULT 3
US-09-949-016-157466
; Sequence 157466, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 157466
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-157466

  Query Match             69.2%;  Score 16.6;  DB 3;  Length 601;
  Best Local Similarity   82.6%;  Pred. No. 1.5e+02;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTA 23
              || |||| | || ||||||||||
Db        273 TCAGAGATGATTTTGAGGGCTTA 295


RESULT 4
US-09-949-016-157573
; Sequence 157573, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 157573
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-157573

  Query Match             69.2%;  Score 16.6;  DB 3;  Length 601;
  Best Local Similarity   82.6%;  Pred. No. 1.5e+02;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTA 23
              || |||| | || ||||||||||
Db        273 TCAGAGATGATTTTGAGGGCTTA 295


RESULT 5
US-09-949-016-198733
; Sequence 198733, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 198733
;   LENGTH: 601
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-198733

  Query Match             69.2%;  Score 16.6;  DB 3;  Length 601;
  Best Local Similarity   82.6%;  Pred. No. 1.5e+02;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTA 23
              ||||  ||||||||| ||||| |
Db        231 TCCGTCACGGTTCTGGGGGCTGA 253


RESULT 6
US-09-949-016-16137
; Sequence 16137, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16137
;   LENGTH: 126176
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-16137

  Query Match             69.2%;  Score 16.6;  DB 3;  Length 126176;
  Best Local Similarity   82.6%;  Pred. No. 2.5e+02;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTA 23
              || ||||  | ||  ||||||||||
Db      72087 TCAGAGATGATTTTGAGGGCTTA 72109


RESULT 7
US-09-949-016-16138
; Sequence 16138, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16138
;   LENGTH: 126176
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-16138

  Query Match             69.2%;  Score 16.6;  DB 3;  Length 126176;
  Best Local Similarity   82.6%;  Pred. No. 2.5e+02;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTA 23
              || ||||  | ||  ||||||||||
Db      72087 TCAGAGATGATTTTGAGGGCTTA 72109


RESULT 8
US-09-949-016-16919
; Sequence 16919, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16919
;   LENGTH: 153866
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-16919

  Query Match             69.2%;  Score 16.6;  DB 3;  Length 153866;
  Best Local Similarity   82.6%;  Pred. No. 2.5e+02;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 CCGAGACGGTTCTGAGGGCTTAC 24
              |||  ||| |||||||||||| |
Db      88075 CCGCCACGATTCTGAGGGCTTCC 88097


RESULT 9
US-09-949-016-16038
; Sequence 16038, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
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;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16038
;   LENGTH: 166698
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(166698)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16038

  Query Match             69.2%;  Score 16.6;  DB 3;  Length 166698;
  Best Local Similarity   82.6%;  Pred. No. 2.5e+02;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTA 23
              || |||| |||||||||||| | |
Db      20937 TCAGAGATGGTTCTGAGGGGTGA 20959


RESULT 10
US-09-949-016-12147/c
; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12147
;   LENGTH: 767677
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(767677)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

  Query Match             69.2%;  Score 16.6;  DB 3;  Length 767677;
  Best Local Similarity   82.6%;  Pred. No. 2.8e+02;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTA 23
              ||||  ||||||||| ||||| |
Db     303242 TCCGTCACGGTTCTGGGGGCTGA 303220


RESULT 11
US-09-949-016-17361/c
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17361
;   LENGTH: 767677
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(767677)
;   OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

  Query Match             69.2%;  Score 16.6;  DB 3;  Length 767677;
  Best Local Similarity   82.6%;  Pred. No. 2.8e+02;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTA 23
              ||||  ||||||||| ||||| |
Db     303242 TCCGTCACGGTTCTGGGGGCTGA 303220


RESULT 12
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             69.2%;  Score 16.6;  DB 3;  Length 4403765;
  Best Local Similarity   82.6%;  Pred. No. 2.4e+02;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTA 23
              |||||||||||| | | |||| ||
Db    2392950 TCCGAGACGGTCCGGCGGGCATA 2392928


RESULT 13
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
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;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match            69.2%;  Score 16.6;  DB 3;  Length 4411529;
  Best Local Similarity  82.6%;  Pred. No. 2.4e+02;
  Matches   19;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTA 23
              ||||||||||| | | |||| ||
Db    2394408 TCCGAGACGGTCCGGCGGGCATA 2394386


RESULT 14
US-09-107-532A-2264
; Sequence 2264, Application US/09107532A
; Patent No. 6583275
;   GENERAL INFORMATION:
;        APPLICANT: Lynn A Doucette-Stamm  and David Bush
;        TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                            ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;        NUMBER OF SEQUENCES: 7310
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;             STREET: 100 Beaver Street
;             CITY: Waltham
;             STATE: Massachusetts
;             COUNTRY: USA
;             ZIP: 02354
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: CD/ROM ISO9660
;             COMPUTER: PC
;             OPERATING SYSTEM: <Unknown>
;             SOFTWARE: ASCII
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/107,532A
;             FILING DATE: 30-Jun-1998
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 60/085,598
;             FILING DATE: 14 May 1998
;             APPLICATION NUMBER: 60/051571
;             FILING DATE: July 2, 1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ariniello, Pamela Deneke
;             REGISTRATION NUMBER: 40,489
;             REFERENCE/DOCKET NUMBER: GTC-012
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (781)893-5007
;             TELEFAX: (781)893-8277
;   INFORMATION FOR SEQ ID NO: 2264:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 921 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: circular
;        MOLECULE TYPE: DNA (genomic)
;        HYPOTHETICAL: NO
;        ANTI-SENSE: NO
;        ORIGINAL SOURCE:
;             ORGANISM: Enterococcus faecium
;        FEATURE:
;             NAME/KEY:  misc_feature
;             LOCATION: (B) LOCATION 1...921
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2264:
US-09-107-532A-2264

  Query Match            67.5%;  Score 16.2;  DB 3;  Length 921;
  Best Local Similarity  85.7%;  Pred. No. 2.4e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GAGACGGTTCTGAGGGCTTAC 24
              ||||||||| ||| ||||| |
Db        533 GAGACGGTTATGACGGCTTCC 553


RESULT 15
US-09-832-496-1
; Sequence 1, Application US/09832496
; Patent No. 6503508
; GENERAL INFORMATION:
;  APPLICANT: Danielsen, Steffen
;  APPLICANT:  Schneider, Palle
;  TITLE OF INVENTION: Polypeptides having haloperoxidase activity
;  FILE REFERENCE: 10042.200-US
;  CURRENT APPLICATION NUMBER: US/09/832,496
;  CURRENT FILING DATE:  2001-04-11
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 1815
;   TYPE: DNA
;   ORGANISM: Dreschlera hartlebii
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1815)
US-09-832-496-1

  Query Match            67.5%;  Score 16.2;  DB 3;  Length 1815;
  Best Local Similarity  85.7%;  Pred. No. 2.6e+02;
  Matches   18;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 CGAGACGGTTCTGAGGGCTTA 23
              || || |||| ||||||||||
Db       1606 CGTGAGGGTTGTGAGGGCTTA 1626


Search completed: December 12, 2005, 00:33:41
Job time : 67.8364 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 00:28:08 ; Search time 304.582 Seconds
(without alignments)
651.599 Million cell updates/sec

Title: US-10-688-489-74
Perfect score: 24
Sequence: 1 tccgagacggttctgagggcttac 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	24	100.0	24	8	US-10-688-489-74	Sequence 74, Appl
	2	24	100.0	24	8	US-10-688-489-75	Sequence 75, Appl
c	3	24	100.0	25	8	US-10-815-480-1	Sequence 1, Appli
	4	24	100.0	25	8	US-10-815-480-2	Sequence 2, Appli
c	5	24	100.0	25	8	US-10-815-480-7	Sequence 7, Appli
c	6	24	100.0	25	8	US-10-815-480-8	Sequence 8, Appli
	7	24	100.0	48	8	US-10-688-489-73	Sequence 73, Appl
	8	24	100.0	51	8	US-10-688-489-84	Sequence 84, Appl
	9	24	100.0	70	8	US-10-688-489-72	Sequence 72, Appl
c	10	24	100.0	98	8	US-10-815-480-71	Sequence 71, Appl
c	11	24	100.0	10945	7	US-10-361-002-5	Sequence 5, Appli
c	12	24	100.0	10945	7	US-10-361-004-5	Sequence 5, Appli
c	13	24	100.0	10975	8	US-10-699-550-1	Sequence 1, Appli
c	14	24	100.0	11029	8	US-10-699-550-2	Sequence 2, Appli
c	15	24	100.0	11029	8	US-10-679-520A-66	Sequence 66, Appl
c	16	24	100.0	11029	9	US-10-706-892-1	Sequence 1, Appli
c	17	24	100.0	11029	9	US-10-985-805-1	Sequence 1, Appli
c	18	24	100.0	11029	9	US-10-956-085-1	Sequence 1, Appli
	19	23	95.8	23	8	US-10-688-489-76	Sequence 76, Appl
	20	23	95.8	50	8	US-10-688-489-85	Sequence 85, Appl
c	21	22.4	93.3	11029	9	US-10-706-892-2	Sequence 2, Appli
	22	22	91.7	22	8	US-10-688-489-77	Sequence 77, Appl
	23	22	91.7	49	8	US-10-688-489-86	Sequence 86, Appl
	24	21	87.5	21	9	US-10-985-805-53	Sequence 53, Appl
	25	21	87.5	23	8	US-10-688-489-149	Sequence 149, App
c	26	19	79.2	19	8	US-10-688-489-116	Sequence 116, App
c	27	19	79.2	87	8	US-10-688-489-101	Sequence 101, App
	28	17.8	74.2	434	7	US-10-425-114-6462	Sequence 6462, Ap
c	29	17.8	74.2	592	4	US-09-925-065A-261547	Sequence 261547,
	30	17.8	74.2	1831	7	US-10-424-599-28488	Sequence 28488, A
c	31	17.6	73.3	1661	6	US-10-225-066A-1045	Sequence 1045, Ap
c	32	17.6	73.3	1661	6	US-10-302-267-29	Sequence 29, Appl
c	33	17.6	73.3	1661	7	US-10-374-780A-2387	Sequence 2387, Ap
c	34	17.6	73.3	1661	7	US-10-412-699B-411	Sequence 411, App
c	35	17.6	73.3	1661	9	US-10-225-066A-1045	Sequence 1045, Ap
c	36	17.6	73.3	1727	7	US-10-425-114-12992	Sequence 12992, A
c	37	17.2	71.7	2060	7	US-10-424-599-83676	Sequence 83676, A
c	38	16.8	70.0	26	8	US-10-815-480-4	Sequence 4, Appli
c	39	16.8	70.0	487	3	US-09-918-995-5377	Sequence 5377, Ap
c	40	16.8	70.0	704	7	US-10-437-963-80309	Sequence 80309, A
	41	16.8	70.0	1416	7	US-10-437-963-21906	Sequence 21906, A
	42	16.8	70.0	2802	7	US-10-261-175A-3	Sequence 3, Appli
	43	16.8	70.0	33488	6	US-10-085-117-235	Sequence 235, App
	44	16.8	70.0	135827	7	US-10-322-281-232	Sequence 232, App
c	45	16.6	69.2	25	7	US-10-719-956-639573	Sequence 639573,

ALIGNMENTS

RESULT 1
US-10-688-489-74
; Sequence 74, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 74
; LENGTH: 24
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-74

Query Match 100.0%; Score 24; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24
||||||||||||||||||||||||
Db 1 TCCGAGACGGTTCTGAGGGCTTAC 24

RESULT 2
US-10-688-489-75
; Sequence 75, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen

```
;  APPLICANT:  Dennis, Geoffrey G.
;  APPLICANT:  Darby, Paul M.
;  TITLE OF INVENTION: Compositions and Methods for Detecting
;  TITLE OF INVENTION:  West Nile Virus
;  FILE REFERENCE: GP140-04.UT
;  CURRENT APPLICATION NUMBER: US/10/688,489
;  CURRENT FILING DATE:  2003-10-16
;  PRIOR APPLICATION NUMBER: 60/418,891
;  PRIOR FILING DATE: 2002-10-16
;  PRIOR APPLICATION NUMBER: 60/429,006
;  PRIOR FILING DATE: 2002-11-25
;  PRIOR APPLICATION NUMBER: 60/449,810
;  PRIOR FILING DATE: 2003-02-24
;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 75
;   LENGTH: 24
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-75

  Query Match             100.0%;  Score 24;  DB 8;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 0.077;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db          1 TCCGAGACGGTTCTGAGGGCTTAC 24


RESULT 3
US-10-815-480-1/c
; Sequence 1, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Karen K. Y.
;  APPLICANT:  Roche Molecular Systems, Inc.
;  TITLE OF INVENTION: Compositions and Methods for Detecting Certain
;  TITLE OF INVENTION:  Flaviviruses, Including Members of the Japanese
;  TITLE OF INVENTION:  Encephalitis Virus Serogroup
;  FILE REFERENCE: 022101-000230US
;  CURRENT APPLICATION NUMBER: US/10/815,480
;  CURRENT FILING DATE:  2004-03-31
;  PRIOR APPLICATION NUMBER: US 60/459,491
;  PRIOR FILING DATE: 2003-03-31
;  PRIOR APPLICATION NUMBER: US 60/552,454
;  PRIOR FILING DATE: 2004-03-12
;  PRIOR APPLICATION NUMBER: US 60/555,530
;  PRIOR FILING DATE: 2004-03-22
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:region of
;   OTHER INFORMATION: conserved sequence in 3' untranslated region of
;   OTHER INFORMATION: the genomes of flaviviruses
US-10-815-480-1

  Query Match             100.0%;  Score 24;  DB 8;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.077;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db         24 TCCGAGACGGTTCTGAGGGCTTAC 1


RESULT 4
US-10-815-480-2
; Sequence 2, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Karen K. Y.
;  APPLICANT:  Roche Molecular Systems, Inc.
;  TITLE OF INVENTION: Compositions and Methods for Detecting Certain
;  TITLE OF INVENTION:  Flaviviruses, Including Members of the Japanese
;  TITLE OF INVENTION:  Encephalitis Virus Serogroup
;  FILE REFERENCE: 022101-000230US
;  CURRENT APPLICATION NUMBER: US/10/815,480
;  CURRENT FILING DATE:  2004-03-31
;  PRIOR APPLICATION NUMBER: US 60/459,491
;  PRIOR FILING DATE: 2003-03-31
;  PRIOR APPLICATION NUMBER: US 60/552,454
;  PRIOR FILING DATE: 2004-03-12
;  PRIOR APPLICATION NUMBER: US 60/555,530
;  PRIOR FILING DATE: 2004-03-22
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:complement to
;   OTHER INFORMATION: SEQ ID NO:1
US-10-815-480-2

  Query Match             100.0%;  Score 24;  DB 8;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.077;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db          2 TCCGAGACGGTTCTGAGGGCTTAC 25


RESULT 5
US-10-815-480-7/c
; Sequence 7, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Karen K. Y.
;  APPLICANT:  Roche Molecular Systems, Inc.
;  TITLE OF INVENTION: Compositions and Methods for Detecting Certain
;  TITLE OF INVENTION:  Flaviviruses, Including Members of the Japanese
;  TITLE OF INVENTION:  Encephalitis Virus Serogroup
;  FILE REFERENCE: 022101-000230US
;  CURRENT APPLICATION NUMBER: US/10/815,480
;  CURRENT FILING DATE:  2004-03-31
;  PRIOR APPLICATION NUMBER: US 60/459,491
;  PRIOR FILING DATE: 2003-03-31
;  PRIOR APPLICATION NUMBER: US 60/552,454
;  PRIOR FILING DATE: 2004-03-12
;  PRIOR APPLICATION NUMBER: US 60/555,530
;  PRIOR FILING DATE: 2004-03-22
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 25
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:Koutango virus
;   OTHER INFORMATION: Primer 1
US-10-815-480-7

  Query Match             100.0%;  Score 24;  DB 8;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 0.077;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db         24 TCCGAGACGGTTCTGAGGGCTTAC 1
```

RESULT 6
US-10-815-480-8/c
; Sequence 8, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
; APPLICANT: Young, Karen K. Y.
; APPLICANT: Roche Molecular Systems, Inc.
; TITLE OF INVENTION: Compositions and Methods for Detecting Certain
; TITLE OF INVENTION: Flaviviruses, Including Members of the Japanese
; TITLE OF INVENTION: Encephalitis Virus Serogroup
; FILE REFERENCE: 022101-000230US
; CURRENT APPLICATION NUMBER: US/10/815,480
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 60/459,491
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/552,454
; PRIOR FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: US 60/555,530
; PRIOR FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Example Primer
; OTHER INFORMATION: 1
US-10-815-480-8

Query Match 100.0%; Score 24; DB 8; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24
||||||||||||||||||||||||
Db 24 TCCGAGACGGTTCTGAGGGCTTAC 1

RESULT 7
US-10-688-489-73
; Sequence 73, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 48
; TYPE: DNA
; ORGANISM: West Nile Virus
US-10-688-489-73

Query Match 100.0%; Score 24; DB 8; Length 48;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24
||||||||||||||||||||||||
Db 1 TCCGAGACGGTTCTGAGGGCTTAC 24

RESULT 8
US-10-688-489-84
; Sequence 84, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 84
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(27)
; OTHER INFORMATION: T7 promoter sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28)...(51)
; OTHER INFORMATION: WNV-complementary sequence
US-10-688-489-84

Query Match 100.0%; Score 24; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGCTTAC 24
||||||||||||||||||||||||
Db 28 TCCGAGACGGTTCTGAGGGCTTAC 51

RESULT 9
US-10-688-489-72
; Sequence 72, Application US/10688489
; Publication No. US20040259108A1
; GENERAL INFORMATION:
; APPLICANT: Linnen, Jeffrey M.
; APPLICANT: Pollner, Reinhold B.
; APPLICANT: Wu, Wen
; APPLICANT: Dennis, Geoffrey G.
; APPLICANT: Darby, Paul M.
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: West Nile Virus
; FILE REFERENCE: GP140-04.UT
; CURRENT APPLICATION NUMBER: US/10/688,489
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/418,891
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: 60/429,006
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/449,810
; PRIOR FILING DATE: 2003-02-24

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;  NUMBER OF SEQ ID NOS: 196
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 72
;   LENGTH: 70
;   TYPE: DNA
;   ORGANISM: West Nile Virus
US-10-688-489-72

  Query Match             100.0%;  Score 24;  DB 8;  Length 70;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db          1 TCCGAGACGGTTCTGAGGGCTTAC 24


RESULT 10
US-10-815-480-71/c
; Sequence 71, Application US/10815480
; Publication No. US20040229261A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Karen K. Y.
;  APPLICANT:  Roche Molecular Systems, Inc.
;  TITLE OF INVENTION: Compositions and Methods for Detecting Certain
;  TITLE OF INVENTION:  Flaviviruses, Including Members of the Japanese
;  TITLE OF INVENTION:  Encephalitis Virus Serogroup
;  FILE REFERENCE: 022101-000230US
;  CURRENT APPLICATION NUMBER: US/10/815,480
;  CURRENT FILING DATE:  2004-03-31
;  PRIOR APPLICATION NUMBER: US 60/459,491
;  PRIOR FILING DATE: 2003-03-31
;  PRIOR APPLICATION NUMBER: US 60/552,454
;  PRIOR FILING DATE: 2004-03-12
;  PRIOR APPLICATION NUMBER: US 60/555,530
;  PRIOR FILING DATE: 2004-03-22
;  NUMBER OF SEQ ID NOS: 74
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
;   LENGTH: 98
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:region of
;   OTHER INFORMATION: conserved sequence in 3' untranslated region of
;   OTHER INFORMATION: the genome of flavivirus AF196835
US-10-815-480-71

  Query Match             100.0%;  Score 24;  DB 8;  Length 98;
  Best Local Similarity   100.0%;  Pred. No. 0.075;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db         68 TCCGAGACGGTTCTGAGGGCTTAC 45


RESULT 11
US-10-361-002-5/c
; Sequence 5, Application US/10361002
; Publication No. US20040170954A1
; GENERAL INFORMATION:
;  APPLICANT: Clearant, Inc.
;  APPLICANT:  McKenney, Keith
;  APPLICANT:  Gillmeister, Lidja
;  APPLICANT:  Marlowe, Kristina
;  APPLICANT:  Armistead, David
;  TITLE OF INVENTION: Pathogen Inactivation Assay
;  FILE REFERENCE: CI-0043
;  CURRENT APPLICATION NUMBER: US/10/361,002
;  CURRENT FILING DATE:  2003-02-10
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 10945
;   TYPE: DNA
;   ORGANISM: West Nile virus
US-10-361-002-5

  Query Match             100.0%;  Score 24;  DB 7;  Length 10945;
  Best Local Similarity   100.0%;  Pred. No. 0.069;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db      10587 TCCGAGACGGTTCTGAGGGCTTAC 10564


RESULT 12
US-10-361-004-5/c
; Sequence 5, Application US/10361004
; Publication No. US20040170981A1
; GENERAL INFORMATION:
;  APPLICANT: Clearant, Inc.
;  APPLICANT:  McKenney, Keith
;  APPLICANT:  Gillmeister, Lidja
;  APPLICANT:  Marlowe, Kristina
;  APPLICANT:  Armistad, David
;  TITLE OF INVENTION: Real-Time Polymerase Chain Reaction Using Large Target Amplicons
;  FILE REFERENCE: CI-0042
;  CURRENT APPLICATION NUMBER: US/10/361,004
;  CURRENT FILING DATE:  2003-02-10
;  NUMBER OF SEQ ID NOS: 99
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
;   LENGTH: 10945
;   TYPE: DNA
;   ORGANISM: West Nile virus
US-10-361-004-5

  Query Match             100.0%;  Score 24;  DB 7;  Length 10945;
  Best Local Similarity   100.0%;  Pred. No. 0.069;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db      10587 TCCGAGACGGTTCTGAGGGCTTAC 10564


RESULT 13
US-10-699-550-1/c
; Sequence 1, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
;  APPLICANT: WONG, SUSAN J.
;  APPLICANT:  SHI, PEI-YONG
;  TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
;  FILE REFERENCE: 454311-2232.1
;  CURRENT APPLICATION NUMBER: US/10/699,550
;  CURRENT FILING DATE:  2003-10-31
;  PRIOR APPLICATION NUMBER: 60/476,513
;  PRIOR FILING DATE: 2003-06-06
;  PRIOR APPLICATION NUMBER: 60/422,755
;  PRIOR FILING DATE: 2002-10-31
;  PRIOR APPLICATION NUMBER: PCT/US02/09036
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: 60/402,860
;  PRIOR FILING DATE: 2002-08-08
;  PRIOR APPLICATION NUMBER: 60/281,947
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/275,025
;  PRIOR FILING DATE: 2001-03-12
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
;   LENGTH: 10975
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;   TYPE: DNA
;   ORGANISM: West Nile virus
US-10-699-550-1

  Query Match             100.0%;  Score 24;  DB 8;  Length 10975;
  Best Local Similarity   100.0%;  Pred. No. 0.069;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db      10611 TCCGAGACGGTTCTGAGGGCTTAC 10588


RESULT 14
US-10-699-550-2/c
; Sequence 2, Application US/10699550
; Publication No. US20040197769A1
; GENERAL INFORMATION:
;  APPLICANT: WONG, SUSAN J.
;  APPLICANT:  SHI, PEI-YONG
;  TITLE OF INVENTION: DIAGNOSTIC TEST FOR WEST NILE VIRUS
;  FILE REFERENCE: 454311-2232.1
;  CURRENT APPLICATION NUMBER: US/10/699,550
;  CURRENT FILING DATE:  2003-10-31
;  PRIOR APPLICATION NUMBER: 60/476,513
;  PRIOR FILING DATE: 2003-06-06
;  PRIOR APPLICATION NUMBER: 60/422,755
;  PRIOR FILING DATE: 2002-10-31
;  PRIOR APPLICATION NUMBER: PCT/US02/09036
;  PRIOR FILING DATE: 2002-03-11
;  PRIOR APPLICATION NUMBER: 60/402,860
;  PRIOR FILING DATE: 2002-08-08
;  PRIOR APPLICATION NUMBER: 60/281,947
;  PRIOR FILING DATE: 2001-04-05
;  PRIOR APPLICATION NUMBER: 60/275,025
;  PRIOR FILING DATE: 2001-03-12
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
;   LENGTH: 11029
;   TYPE: DNA
;   ORGANISM: West Nile virus
US-10-699-550-2

  Query Match             100.0%;  Score 24;  DB 8;  Length 11029;
  Best Local Similarity   100.0%;  Pred. No. 0.069;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db      10629 TCCGAGACGGTTCTGAGGGCTTAC 10606


RESULT 15
US-10-679-520A-66/c
; Sequence 66, Application US/10679520A
; Publication No. US20050031641A1
; GENERAL INFORMATION:
;  APPLICANT: LOOSMORE, SHEENA MAY
;  APPLICANT:  AUDONNET, JEAN-CHRISTOPHE FRANCIS
;  APPLICANT:  MINKE, JULES MAARTEN
;  TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
;  FILE REFERENCE: 574313-3161.4
;  CURRENT APPLICATION NUMBER: US/10/679,520A
;  CURRENT FILING DATE:  2003-10-06
;  PRIOR APPLICATION NUMBER: 10/374,953
;  PRIOR FILING DATE: 2003-02-26
;  PRIOR APPLICATION NUMBER: 10/116,298
;  PRIOR FILING DATE: 2002-04-04
;  PRIOR APPLICATION NUMBER: 60/281,923
;  PRIOR FILING DATE: 2001-04-06
;  PRIOR APPLICATION NUMBER: PCT/FR02/01200
;  PRIOR FILING DATE: 2002-04-05
;  PRIOR APPLICATION NUMBER: FR 01/04737
;  PRIOR FILING DATE: 2001-04-06
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
;   LENGTH: 11029
;   TYPE: DNA
;   ORGANISM: West Nile virus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (97)..(10395)
US-10-679-520A-66

  Query Match             100.0%;  Score 24;  DB 8;  Length 11029;
  Best Local Similarity   100.0%;  Pred. No. 0.069;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db      10629 TCCGAGACGGTTCTGAGGGCTTAC 10606


Search completed: December 12, 2005, 02:19:38
Job time : 305.582 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 00:31:12 ; Search time 92.5091 Seconds
(without alignments)
96.991 Million cell updates/sec

Title: US-10-688-489-74
Perfect score: 24
Sequence: 1 tccgagacggttctgagggcttac 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3392430 seqs, 186927314 residues

Total number of hits satisfying chosen parameters: 6784860

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	24	100.0	11029	6	US-10-714-781A-66	Sequence 66, Appl
c 2	16.8	70.0	1509	6	US-10-750-185-26120	Sequence 26120, A
3	16.8	70.0	1692	6	US-10-750-185-60065	Sequence 60065, A
4	16	66.7	1138	6	US-10-750-185-59175	Sequence 59175, A
c 5	16	66.7	2259	7	US-11-000-463-39	Sequence 39, Appl
6	15.6	65.0	4252	6	US-10-750-185-59992	Sequence 59992, A
c 7	15.6	65.0	5371	6	US-10-821-234-274	Sequence 274, App
8	15.6	65.0	5390	6	US-10-849-438-4	Sequence 4, Appli
9	15.6	65.0	135019	6	US-10-849-438-11	Sequence 11, Appl
c 10	15.6	65.0	151169	7	US-11-121-086-38	Sequence 38, Appl
11	15.4	64.2	19	8	US-11-101-244-668857	Sequence 668857,
12	15.4	64.2	19	9	US-11-083-784-668857	Sequence 668857,
c 13	15.4	64.2	20	6	US-10-849-438-42	Sequence 42, Appl
14	15.2	63.3	429	6	US-10-467-657-273	Sequence 273, App
15	15.2	63.3	429	6	US-10-467-657-3719	Sequence 3719, Ap
c 16	15.2	63.3	600	6	US-10-750-185-83	Sequence 83, Appl
c 17	15.2	63.3	600	6	US-10-750-185-2361	Sequence 2361, Ap
c 18	15.2	63.3	600	6	US-10-750-185-2446	Sequence 2446, Ap
c 19	15.2	63.3	1302	6	US-10-750-185-58252	Sequence 58252, A
c 20	15.2	63.3	1414	6	US-10-750-185-44989	Sequence 44989, A
21	15.2	63.3	1551	6	US-10-750-185-36404	Sequence 36404, A
c 22	15.2	63.3	1665	7	US-11-102-240-85	Sequence 85, Appl
c 23	15.2	63.3	1939	7	US-11-000-463-164	Sequence 164, App
c 24	15.2	63.3	1944	7	US-11-000-463-636	Sequence 636, App
c 25	15.2	63.3	2141	6	US-10-750-185-46042	Sequence 46042, A
c 26	15.2	63.3	2327	6	US-10-750-185-47722	Sequence 47722, A
c 27	15.2	63.3	2478	7	US-11-075-046-47	Sequence 47, Appl
c 28	15.2	63.3	2478	7	US-11-075-046-49	Sequence 49, Appl
c 29	15.2	63.3	2479	7	US-11-075-046-51	Sequence 51, Appl
c 30	15.2	63.3	2748	6	US-10-821-234-662	Sequence 662, App
c 31	15.2	63.3	120096	7	US-11-121-086-24	Sequence 24, Appl
c 32	15	62.5	1516	6	US-10-750-185-35820	Sequence 35820, A
33	15	62.5	2541	6	US-10-750-185-42703	Sequence 42703, A
34	15	62.5	19959	6	US-10-993-516-1	Sequence 1, Appli
35	15	62.5	149419	7	US-11-112-908-49	Sequence 49, Appl
36	15	62.5	157224	7	US-11-112-908-51	Sequence 51, Appl
37	15	62.5	160170	7	US-11-121-086-32	Sequence 32, Appl
38	15	62.5	161726	7	US-11-112-908-48	Sequence 48, Appl
39	15	62.5	161726	7	US-11-112-908-52	Sequence 52, Appl
c 40	14.8	61.7	276	6	US-10-467-657-3455	Sequence 3455, Ap
41	14.8	61.7	276	6	US-10-467-657-4805	Sequence 4805, Ap
42	14.8	61.7	1105	6	US-10-750-185-40960	Sequence 40960, A
43	14.8	61.7	163162	7	US-11-121-086-66	Sequence 66, Appl
44	14.6	60.8	984	6	US-10-750-185-61751	Sequence 61751, A
45	14.6	60.8	1136	6	US-10-750-185-50493	Sequence 50493, A

ALIGNMENTS

RESULT 1
US-10-714-781A-66/c
; Sequence 66, Application US/10714781A
; Publication No. US20050255127A1
; GENERAL INFORMATION:
; APPLICANT: LOOSMORE, SHEENA MAY
; APPLICANT: MINKE, JULES MAARTEN
; TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST WEST NILE VIRUS
; FILE REFERENCE: 574313-3161.5
; CURRENT APPLICATION NUMBER: US/10/714,781A
; CURRENT FILING DATE: 2003-11-17
; PRIOR APPLICATION NUMBER: 10/679,520
; PRIOR FILING DATE: 2003-10-06
; PRIOR APPLICATION NUMBER: 10/374,953
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 10/116,298
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,923
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 10/676,502
; PRIOR FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: PCT/FR02/01200
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
; LENGTH: 11029
; TYPE: DNA
; ORGANISM: West Nile virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (97)..(10395)
US-10-714-781A-66

Query Match 100.0%; Score 24; DB 6; Length 11029;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              ||||||||||||||||||||||||
Db      10629 TCCGAGACGGTTCTGAGGGCTTAC 10606
```

RESULT 2
US-10-750-185-26120/c
; Sequence 26120, Application US/10750185

```
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 26120
;   LENGTH: 1509
;   TYPE: DNA
;   ORGANISM: Bovine  19866881160878
US-10-750-185-26120

  Query Match             70.0%;  Score 16.8;  DB 6;  Length 1509;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CCGAGACGGTTCTGAGGGCT 21
              ||||| |||||||| |||||
Db        359 CCGAGGCGGTTCTGCGGGCT 340


RESULT 3
US-10-750-185-60065
; Sequence 60065, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 60065
;   LENGTH: 1692
;   TYPE: DNA
;   ORGANISM: Bovine  19866880728422
US-10-750-185-60065

  Query Match             70.0%;  Score 16.8;  DB 6;  Length 1692;
  Best Local Similarity   90.0%;  Pred. No. 22;
  Matches   18;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGC 20
              ||| ||||| ||||||||||
Db        677 TCCCAGACGCTTCTGAGGGC 696


RESULT 4
US-10-750-185-59175
; Sequence 59175, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 59175
;   LENGTH: 1138
;   TYPE: DNA
;   ORGANISM: Bovine  19866880752265
US-10-750-185-59175

  Query Match             66.7%;  Score 16;  DB 6;  Length 1138;
  Best Local Similarity   79.2%;  Pred. No. 53;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              || |||||| ||||||| ||| |
Db       1039 TCAGAGACGATTCTGAGCACTTTC 1062


RESULT 5
US-11-000-463-39/c
; Sequence 39, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Chen, Rui-hong
;  APPLICANT:  Qian, Xiaohong B.
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Cao, Yi-Cheng
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
;  FILE REFERENCE: 785CIP4CN
;  CURRENT APPLICATION NUMBER: US/11/000,463
;  CURRENT FILING DATE:  2004-11-29
;  PRIOR APPLICATION NUMBER: 10/291,265
;  PRIOR FILING DATE: 2002-11-08
;  PRIOR APPLICATION NUMBER: PCT/US01/02623
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: 09/922,279
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 09/617,746
;  PRIOR FILING DATE: 2000-07-17
;  PRIOR APPLICATION NUMBER: 09/631,451
;  PRIOR FILING DATE: 2000-08-03
;  PRIOR APPLICATION NUMBER: 09/633,870
;  PRIOR FILING DATE: 2000-09-15
;  NUMBER OF SEQ ID NOS: 944
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 39
;   LENGTH: 2259
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (182)..(1078)
US-11-000-463-39
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  Query Match             66.7%;  Score 16;  DB 7;  Length 2259;
  Best Local Similarity   79.2%;  Pred. No. 55;
  Matches   19;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTTAC 24
              |||| | ||||||  | |||||||
Db         53 TCCGGGGCGGTTCGCAAGGCTTAC 30


RESULT 6
US-10-750-185-59992
; Sequence 59992, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 59992
;   LENGTH: 4252
;   TYPE: DNA
;   ORGANISM: Bovine  19866881275597
US-10-750-185-59992

  Query Match             65.0%;  Score 15.6;  DB 6;  Length 4252;
  Best Local Similarity   81.8%;  Pred. No. 88;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 CCGAGACGGTTCTGAGGGCTTA 23
              | |||| ||| |||||||| ||
Db       2957 CAGAGAAGGTGCTGAGGGCATA 2978


RESULT 7
US-10-821-234-274/c
; Sequence 274, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 274
;   LENGTH: 5371
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-821-234-274

  Query Match             65.0%;  Score 15.6;  DB 6;  Length 5371;
  Best Local Similarity   81.8%;  Pred. No. 89;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 CCGAGACGGTTCTGAGGGCTTA 23
              ||    | |||||||||||||||
Db       4332 CCAGAATGGTTCTGAGGGCTTA 4311


RESULT 8
US-10-849-438-4
; Sequence 4, Application US/10849438
; Publication No. US20050261217A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Bridget Lollo
;  TITLE OF INVENTION: MODULATION OF PUMILIO 1 EXPRESSION
;  FILE REFERENCE: RTS-0715US
;  CURRENT APPLICATION NUMBER: US/10/849,438
;  CURRENT FILING DATE:  2004-05-18
;  NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 4
;   LENGTH: 5390
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (96)...(3656)
US-10-849-438-4

  Query Match             65.0%;  Score 15.6;  DB 6;  Length 5390;
  Best Local Similarity   81.8%;  Pred. No. 89;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 CCGAGACGGTTCTGAGGGCTTA 23
              ||    | |||||||||||||||
Db       1040 CCAGAATGGTTCTGAGGGCTTA 1061


RESULT 9
US-10-849-438-11
; Sequence 11, Application US/10849438
; Publication No. US20050261217A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Bridget Lollo
;  TITLE OF INVENTION: MODULATION OF PUMILIO 1 EXPRESSION
;  FILE REFERENCE: RTS-0715US
;  CURRENT APPLICATION NUMBER: US/10/849,438
;  CURRENT FILING DATE:  2004-05-18
;  NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 11
;   LENGTH: 135019
;   TYPE: DNA
;   ORGANISM: H. sapiens
US-10-849-438-11

  Query Match             65.0%;  Score 15.6;  DB 6;  Length 135019;
  Best Local Similarity   81.8%;  Pred. No. 1e+02;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 CCGAGACGGTTCTGAGGGCTTA 23
              ||    | |||||||||||||||
Db      73522 CCAGAATGGTTCTGAGGGCTTA 73543


RESULT 10
US-11-121-086-38/c
; Sequence 38, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
;  APPLICANT: POULSEN, TIM S.
;  APPLICANT:  NIELSEN, KIRSTEN V.
;  TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
;  FILE REFERENCE: 09138.6000-00000
;  CURRENT APPLICATION NUMBER: US/11/121,086
;  CURRENT FILING DATE:  2005-05-04
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;  PRIOR APPLICATION NUMBER: 60/567,570
;  PRIOR FILING DATE: 2004-05-04
;  NUMBER OF SEQ ID NOS: 107
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 38
;   LENGTH: 151169
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-121-086-38

  Query Match            65.0%;  Score 15.6;  DB 7;  Length 151169;
  Best Local Similarity   81.8%;  Pred. No. 1e+02;
  Matches   18;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 TCCGAGACGGTTCTGAGGGCTT 22
              ||  ||| | ||||||||||||
Db      30253 TCTAAGATGTTTCTGAGGGCTT 30232


RESULT 11
US-11-101-244-668857
; Sequence 668857, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/101,244
;  CURRENT FILING DATE:  2005-04-07
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 668857
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-101-244-668857

  Query Match            64.2%;  Score 15.4;  DB 8;  Length 19;
  Best Local Similarity   64.7%;  Pred. No. 86;
  Matches   11;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ACGGTTCTGAGGGCTTA 23
              | ||::|:||||||::|
Db          3 AUGGUUCUGAGGGCUUA 19


RESULT 12
US-11-083-784-668857
; Sequence 668857, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
;  APPLICANT: Dharmacon, Inc.
;  APPLICANT:  Khvorova, Anastasia
;  APPLICANT:  Reynolds, Angela
;  APPLICANT:  Leake, Devin
;  APPLICANT:  Marshall, William
;  APPLICANT:  Scaringe, Stephen
;  TITLE OF INVENTION: Functional and Hyperfunctional siRNA
;  FILE REFERENCE: 13499US
;  CURRENT APPLICATION NUMBER: US/11/083,784
;  CURRENT FILING DATE:  2005-03-18
;  PRIOR APPLICATION NUMBER: US/10/714,333
;  PRIOR FILING DATE: 2003-11-14
;  PRIOR APPLICATION NUMBER: 60/502,050
;  PRIOR FILING DATE: 2003-09-10
;  PRIOR APPLICATION NUMBER: 60/426,137
;  PRIOR FILING DATE: 2002-11-14
;  NUMBER OF SEQ ID NOS: 1591911
;  SOFTWARE: Proprietary
; SEQ ID NO 668857
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-11-083-784-668857

  Query Match            64.2%;  Score 15.4;  DB 9;  Length 19;
  Best Local Similarity   64.7%;  Pred. No. 86;
  Matches   11;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ACGGTTCTGAGGGCTTA 23
              | ||::|:||||||::|
Db          3 AUGGUUCUGAGGGCUUA 19


RESULT 13
US-10-849-438-42/c
; Sequence 42, Application US/10849438
; Publication No. US20050261217A1
; GENERAL INFORMATION:
;  APPLICANT: Kenneth W. Dobie
;  APPLICANT:  Bridget Lollo
;  TITLE OF INVENTION: MODULATION OF PUMILIO 1 EXPRESSION
;  FILE REFERENCE: RTS-0715US
;  CURRENT APPLICATION NUMBER: US/10/849,438
;  CURRENT FILING DATE:  2004-05-18
;  NUMBER OF SEQ ID NOS: 123
; SEQ ID NO 42
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Compound
US-10-849-438-42

  Query Match            64.2%;  Score 15.4;  DB 6;  Length 20;
  Best Local Similarity   94.1%;  Pred. No. 86;
  Matches   16;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ACGGTTCTGAGGGCTTA 23
              | ||||||||||||||||
Db         19 ATGGTTCTGAGGGCTTA 3


RESULT 14
US-10-467-657-273
; Sequence 273, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 273
;   LENGTH: 429
;   TYPE: DNA
;   ORGANISM: Neisseria gonorrhoeae
US-10-467-657-273
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Query Match 63.3%; Score 15.2; DB 6; Length 429;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 TCCGAGACGGTTCTGAGGGC 20
              ||||| |||| | |||||||
Db          7 TCCGAAACGGATTTGAGGGC 26
```

RESULT 15
US-10-467-657-3719
; Sequence 3719, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3719
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3719

Query Match 63.3%; Score 15.2; DB 6; Length 429;
Best Local Similarity 85.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCGAGACGGTTCTGAGGGC 20
||||| |||| | |||||||
Db 7 TCCGAAACGGATTTGAGGGC 26

Search completed: December 12, 2005, 02:23:15
Job time : 92.5091 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 12, 2005, 03:28:33 ; Search time 372 Seconds
(without alignments)
24.120 Million cell updates/sec

Title: US-10-688-489-74
Perfect score: 24
Sequence: 1 tccgagacggttctgagggcttac 24

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 3392430 seqs, 186927314 residues

Word size : 0

Total number of hits satisfying chosen parameters: 19364

Minimum DB seq length: 22
Maximum DB seq length: 24

Post-processing: Listing first 45 summaries

Database : Published_Applications_NA_New:*
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3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	10	41.7	23	7	US-11-186-497-19	Sequence 19, Appl
c 2	9	37.5	22	6	US-10-750-185-10657	Sequence 10657, A
c 3	9	37.5	22	7	US-11-069-908-2047	Sequence 2047, Ap
c 4	9	37.5	22	7	US-11-069-908-4146	Sequence 4146, Ap
5	9	37.5	22	7	US-11-069-908-4852	Sequence 4852, Ap
6	9	37.5	22	7	US-11-069-908-5595	Sequence 5595, Ap
7	9	37.5	23	7	US-11-072-031-2	Sequence 2, Appli
c 8	8	33.3	22	6	US-10-500-831-32	Sequence 32, Appl
c 9	8	33.3	22	6	US-10-500-831-185	Sequence 185, App
10	8	33.3	22	6	US-10-477-950-12	Sequence 12, Appl
11	8	33.3	22	6	US-10-524-643-91	Sequence 91, Appl
c 12	8	33.3	22	6	US-10-750-185-10054	Sequence 10054, A
13	8	33.3	22	6	US-10-750-185-11416	Sequence 11416, A
c 14	8	33.3	22	6	US-10-750-185-11416	Sequence 11416, A
c 15	8	33.3	22	6	US-10-750-185-12782	Sequence 12782, A
16	8	33.3	22	6	US-10-750-185-13800	Sequence 13800, A
17	8	33.3	22	7	US-11-102-228-6	Sequence 6, Appli
c 18	8	33.3	22	7	US-11-069-908-374	Sequence 374, App
c 19	8	33.3	22	7	US-11-069-908-1363	Sequence 1363, Ap
c 20	8	33.3	22	7	US-11-069-908-1475	Sequence 1475, Ap
c 21	8	33.3	22	7	US-11-069-908-1780	Sequence 1780, Ap
c 22	8	33.3	22	7	US-11-069-908-3729	Sequence 3729, Ap
c 23	8	33.3	22	7	US-11-069-908-3841	Sequence 3841, Ap
c 24	8	33.3	22	7	US-11-069-908-4413	Sequence 4413, Ap
25	8	33.3	22	7	US-11-069-908-5076	Sequence 5076, Ap
c 26	8	33.3	22	7	US-11-069-908-6891	Sequence 6891, Ap
c 27	8	33.3	22	7	US-11-069-908-6954	Sequence 6954, Ap
c 28	8	33.3	22	7	US-11-083-538-12	Sequence 12, Appl
c 29	8	33.3	23	6	US-10-750-185-12555	Sequence 12555, A
c 30	8	33.3	23	6	US-10-750-185-13190	Sequence 13190, A
31	8	33.3	23	6	US-10-750-185-14244	Sequence 14244, A
32	8	33.3	23	6	US-10-750-185-14506	Sequence 14506, A
33	8	33.3	23	6	US-10-750-185-14794	Sequence 14794, A
34	8	33.3	23	6	US-10-750-185-16082	Sequence 16082, A
35	8	33.3	23	7	US-11-043-959-30	Sequence 30, Appl
36	8	33.3	23	7	US-11-052-544-23	Sequence 23, Appl
c 37	8	33.3	23	7	US-11-049-830-1	Sequence 1, Appli
38	8	33.3	23	7	US-11-072-031-47	Sequence 47, Appl
c 39	8	33.3	23	7	US-11-072-031-185	Sequence 185, App
40	8	33.3	23	7	US-11-090-739-106	Sequence 106, App
c 41	8	33.3	23	7	US-11-069-908-2020	Sequence 2020, Ap
c 42	8	33.3	23	7	US-11-069-908-4386	Sequence 4386, Ap
43	8	33.3	23	9	US-11-096-706-218	Sequence 218, App
c 44	8	33.3	24	6	US-10-500-831-9	Sequence 9, Appli
c 45	8	33.3	24	6	US-10-500-831-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-11-186-497-19/c
; Sequence 19, Application US/11186497
; Publication No. US20050255597A1
; GENERAL INFORMATION:
; APPLICANT: Naldini, Luigi
; APPLICANT: Dull, Thomas
; APPLICANT: Farson, Deborah A.
; APPLICANT: Witt, Rochelle
; TITLE OF INVENTION: METHOD AND MEANS FOR PRODUCING HIGH
; TITLE OF INVENTION: TITER, SAFE, RECOMBINANT LENTIVIRUS VECTORS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/186,497
; FILING DATE: 21-JULY-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/271,365
; FILING DATE: 18-Mar-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/989,394
; FILING DATE: 12-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Nakamura, Dean H.
; REGISTRATION NUMBER: 33,981
; REFERENCE/DOCKET NUMBER: A7086
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)293-7060
; TELEFAX: (202)293-7860
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 base pairs
; TYPE: nucleic acid

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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-11-186-497-19

  Query Match             41.7%;  Score 10;  DB 7;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 2.7e+03;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGGCT 21
              ||||||||||
Db         21 TCTGAGGGCT 12


RESULT 2
US-10-750-185-10657/c
; Sequence 10657, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 10657
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Reverse Primer
US-10-750-185-10657

  Query Match             37.5%;  Score 9;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTCTGAGG 18
              |||||||||
Db         10 GTTCTGAGG 2


RESULT 3
US-11-069-908-2047/c
; Sequence 2047, Application US/11069908
; Publication No. US20050266432A1
; GENERAL INFORMATION:
;  APPLICANT: OLIPHANT, ARNOLD
;  APPLICANT:  MURRAY, SARAH
;  TITLE OF INVENTION: HAPLOTYPE MARKERS FOR DIAGNOSING SUSCEPTIBILITY TO IMMUNOLOGICAL
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 029011-0402
;  CURRENT APPLICATION NUMBER: US/11/069,908
;  CURRENT FILING DATE:  2005-02-28
;  PRIOR APPLICATION NUMBER: 60/547,823
;  PRIOR FILING DATE: 2004-02-26
;  NUMBER OF SEQ ID NOS: 7098
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2047
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-11-069-908-2047

  Query Match             37.5%;  Score 9;  DB 7;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 TCTGAGGGC 20
              |||||||||
Db         22 TCTGAGGGC 14


RESULT 4
US-11-069-908-4146/c
; Sequence 4146, Application US/11069908
; Publication No. US20050266432A1
; GENERAL INFORMATION:
;  APPLICANT: OLIPHANT, ARNOLD
;  APPLICANT:  MURRAY, SARAH
;  TITLE OF INVENTION: HAPLOTYPE MARKERS FOR DIAGNOSING SUSCEPTIBILITY TO IMMUNOLOGICAL
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 029011-0402
;  CURRENT APPLICATION NUMBER: US/11/069,908
;  CURRENT FILING DATE:  2005-02-28
;  PRIOR APPLICATION NUMBER: 60/547,823
;  PRIOR FILING DATE: 2004-02-26
;  NUMBER OF SEQ ID NOS: 7098
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4146
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-11-069-908-4146

  Query Match             37.5%;  Score 9;  DB 7;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CGGTTCTGA 16
              |||||||||
Db         22 CGGTTCTGA 14


RESULT 5
US-11-069-908-4852
; Sequence 4852, Application US/11069908
; Publication No. US20050266432A1
; GENERAL INFORMATION:
;  APPLICANT: OLIPHANT, ARNOLD
;  APPLICANT:  MURRAY, SARAH
;  TITLE OF INVENTION: HAPLOTYPE MARKERS FOR DIAGNOSING SUSCEPTIBILITY TO IMMUNOLOGICAL
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 029011-0402
;  CURRENT APPLICATION NUMBER: US/11/069,908
;  CURRENT FILING DATE:  2005-02-28
;  PRIOR APPLICATION NUMBER: 60/547,823
;  PRIOR FILING DATE: 2004-02-26
;  NUMBER OF SEQ ID NOS: 7098
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4852
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-11-069-908-4852

  Query Match             37.5%;  Score 9;  DB 7;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         13 CTGAGGGCT 21
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              |||||||||
Db          3 CTGAGGGCT 11


RESULT 6
US-11-069-908-5595
; Sequence 5595, Application US/11069908
; Publication No. US20050266432A1
; GENERAL INFORMATION:
;  APPLICANT: OLIPHANT, ARNOLD
;  APPLICANT:  MURRAY, SARAH
;  TITLE OF INVENTION: HAPLOTYPE MARKERS FOR DIAGNOSING SUSCEPTIBILITY TO IMMUNOLOGICAL
;  TITLE OF INVENTION:  CONDITIONS
;  FILE REFERENCE: 029011-0402
;  CURRENT APPLICATION NUMBER: US/11/069,908
;  CURRENT FILING DATE:  2005-02-28
;  PRIOR APPLICATION NUMBER: 60/547,823
;  PRIOR FILING DATE: 2004-02-26
;  NUMBER OF SEQ ID NOS: 7098
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5595
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic oligonucleotide
US-11-069-908-5595

  Query Match             37.5%;  Score 9;  DB 7;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TTCTGAGGG 19
              |||||||||
Db         12 TTCTGAGGG 20


RESULT 7
US-11-072-031-2
; Sequence 2, Application US/11072031
; Publication No. US20050261222A1
; GENERAL INFORMATION:
;  APPLICANT: Beiersdorf AG, Hamburg
;  APPLICANT:  Wolber, Rainer
;  APPLICANT:  Kolbe, Ludger
;  APPLICANT:  Mundt, Claudia
;  APPLICANT:  Gallinat, Stefan
;  APPLICANT:  Breitenbach, Ute
;  TITLE OF INVENTION: Oligonucleotides for the Treatment of Irritative or Inflammatory
;  TITLE OF INVENTION:  Symptoms Through RNA Interference
;  FILE REFERENCE: 104035/269168
;  CURRENT APPLICATION NUMBER: US/11/072,031
;  CURRENT FILING DATE:  2005-03-03
;  PRIOR APPLICATION NUMBER: DE 102004010547.2
;  PRIOR FILING DATE: 2004-03-03
;  NUMBER OF SEQ ID NOS: 194
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 23
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-072-031-2

  Query Match             37.5%;  Score 9;  DB 7;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 1e+04;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GAGACGGTT 12
              |||||||||
Db         15 GAGACGGTT 23


RESULT 8
US-10-500-831-32/c
; Sequence 32, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
;  APPLICANT: Frank KARLSEN
;  TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
;  FILE REFERENCE: B0192.70052US00
;  CURRENT APPLICATION NUMBER: US/10/500,831
;  CURRENT FILING DATE:  2004-07-07
;  PRIOR APPLICATION NUMBER: GB 0200258.2
;  PRIOR FILING DATE: 2002-01-07
;  PRIOR APPLICATION NUMBER: GB 0214124.0
;  PRIOR FILING DATE: 2002-06-19
;  NUMBER OF SEQ ID NOS: 387
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Human papillomavirus type 31
US-10-500-831-32

  Query Match             33.3%;  Score 8;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CGGTTCTG 15
              ||||||||
Db         14 CGGTTCTG 7


RESULT 9
US-10-500-831-185/c
; Sequence 185, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
;  APPLICANT: Frank KARLSEN
;  TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
;  FILE REFERENCE: B0192.70052US00
;  CURRENT APPLICATION NUMBER: US/10/500,831
;  CURRENT FILING DATE:  2004-07-07
;  PRIOR APPLICATION NUMBER: GB 0200258.2
;  PRIOR FILING DATE: 2002-01-07
;  PRIOR APPLICATION NUMBER: GB 0214124.0
;  PRIOR FILING DATE: 2002-06-19
;  NUMBER OF SEQ ID NOS: 387
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 185
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Human papillomavirus type 31
US-10-500-831-185

  Query Match             33.3%;  Score 8;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 CGGTTCTG 15
              ||||||||
Db         14 CGGTTCTG 7


RESULT 10
US-10-477-950-12
; Sequence 12, Application US/10477950
; Publication No. US20050260207A1
; GENERAL INFORMATION:
;  APPLICANT: Krka tovarna zdravil, d.d., Novo mesto
;  TITLE OF INVENTION: Monoclonal antibody neutralising Cathepsin B activity
;  TITLE OF INVENTION:  and uses thereof
;  FILE REFERENCE: 28880
;  CURRENT APPLICATION NUMBER: US/10/477,950
;  CURRENT FILING DATE:  2003-11-18
;  PRIOR APPLICATION NUMBER: SI/P200100132
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;  PRIOR FILING DATE: 2001-05-18
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Mouse
US-10-477-950-12

  Query Match             33.3%;  Score 8;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 GAGACGGT 11
              ||||||||
Db         15 GAGACGGT 22


RESULT 11
US-10-524-643-91
; Sequence 91, Application US/10524643
; Publication No. US20050261215A1
; GENERAL INFORMATION:
;  APPLICANT: GARREN, Hideki
;  APPLICANT:  HO, Peggy P.
;  APPLICANT:  STEINMAN, Lawrence
;  TITLE OF INVENTION: METHODS AND IMMUNE MODULATORY NUCLEIC ACID COMPOSITIONS FOR
;  TITLE OF INVENTION:  PREVENTING AND TREATING DISEASE
;  FILE REFERENCE: 022259-001010US
;  CURRENT APPLICATION NUMBER: US/10/524,643
;  CURRENT FILING DATE:  2005-02-10
;  PRIOR APPLICATION NUMBER: PCT/US2003/037157
;  PRIOR FILING DATE: 2003-11-21
;  NUMBER OF SEQ ID NOS: 296
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 91
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: immunomodulatory oligonucleotide
US-10-524-643-91

  Query Match             33.3%;  Score 8;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         14 TGAGGGCT 21
              ||||||||
Db          7 TGAGGGCT 14


RESULT 12
US-10-750-185-10054/c
; Sequence 10054, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 10054
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Reverse Primer
US-10-750-185-10054

  Query Match             33.3%;  Score 8;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 AGGGCTTA 23
              ||||||||
Db         18 AGGGCTTA 11


RESULT 13
US-10-750-185-11416
; Sequence 11416, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 11416
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Reverse Primer
US-10-750-185-11416

  Query Match             33.3%;  Score 8;  DB 6;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 4e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GTTCTGAG 17
              ||||||||
Db          1 GTTCTGAG 8


RESULT 14
US-10-750-185-11416/c
; Sequence 11416, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
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; SEQ ID NO 11416
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Reverse Primer
US-10-750-185-11416

  Query Match            33.3%;  Score 8;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 4e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TCCGAGAC 8
              ||||||||
Db         15 TCCGAGAC 8


RESULT 15
US-10-750-185-12782/c
; Sequence 12782, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 12782
;   LENGTH: 22
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   OTHER INFORMATION: Reverse Primer
US-10-750-185-12782

  Query Match            33.3%;  Score 8;  DB 6;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 4e+04;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         11 TTCTGAGG 18
              ||||||||
Db         14 TTCTGAGG 7


Search completed: December 12, 2005, 04:33:49
Job time : 372 secs
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